OM protein - protein search, using sw model
Run on: May 12, 2006, 20:33:31 ; Search time 187 Seconds
                                                                  (without alignments)
                                        549.811 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSQSSHA.........EAGSEEAEEKQDSEKPLLEL 234
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 243163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 0%
Database :   A_Geneseq 21:*
                  Listing first 1500 summaries
                  1: geneseqp1980s:*
                  2: geneseqp1990s:*
                  3: geneseqp2000s:*
                  4: geneseqp2001s:*
                  5: geneseqp2002s:*
                  6: geneseqp2003as:*
                  7: geneseqp2003bs:*
                  8: geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                  SUMMARIES

No.   Score   Match Length DB ID   Description

RESULT 1
ID   AAU29056 standard; protein; 234 AA.
DE   Human PRO polypeptide sequence #33.
PN   WO20016848-A2.
PD   20-SEP-2001.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 2
ID   AAM39929 standard; protein; 234 AA.
DE   Human polypeptide SEQ ID NO 3074.
PN   WO20015331-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 3
ID   AAB87532 standard; protein; 234 AA.
DE   Human PRO1864.
PN   WO20016318-A2.
PD   08-MAR-2001.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 4
ID   ABG95857 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein sequence SEQ ID NO:62.
PN   US20021119130-A1.
PD   29-AUG-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 5
ID   ABB84847 standard; protein; 234 AA.
DE   Human PRO1864 protein sequence SEQ ID NO:62.
PN   WO20020690-A2.
PD   03-JAN-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 6
ID   ABB95453 standard; protein; 234 AA.
DE   Human angiogenesis related protein PRO1864 SEQ ID NO: 62.

PN   WO20020284-A2.
PD   31-JAN-2002.
PA   (GETH) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match   100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 7
ID   ABU58432 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030272272-A1.
PD   06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 8
ID   ABU87980 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030312127-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 9
ID   ABU84295 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030312212-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 10
ID   ABR66169 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030276159-A1.
PD   20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 11
ID   ABR65559 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030400070-A1.
PD   27-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 12
ID   ABU99499 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030312113-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 13
ID   ABU82738 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein #33.
PN   US20030324070-A1.
PD   27-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 14
ID   ABU89859 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030336147-A1.

PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 15
ID   ABR68108 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027264-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 16
ID   ABU96161 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036144-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 17
ID   ABU92592 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036149-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 18
ID   ABO08669 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044923-A1.
PD   06-MAR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 19
ID   ABO02721 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040062-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 20
ID   ABR74875 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040056-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 21
ID   ABR94637 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044926-A1.
PD   06-MAR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 22
ID   ABU85610 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036140-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 23
ID   ABU98770 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003013153-A1.
PD   16-JAN-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 24
ID   ABU97985 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003017544-A1.
PD   23-JAN-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;

     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 25
ID   ABU91691 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003027277-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 26
ID   ABU89384 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036141-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 27
ID   ABU86225 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 28
ID   ABU67438 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 29
ID   ABU80466 standard; protein; 234 AA.
DE   Human PRO protein #33.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 30
ID   ABU90882 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003018173-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 31
ID   ABO33941 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO1864.
PN   US2003009013-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 32
ID   ABR99384 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040063-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 33
ID   ABR98774 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040064-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
RESULT 34
ID   ABO16297 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003027267-A1.

RESULT 35
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABR92197 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030036160-A1.
PD 20-FEB-2003.

RESULT 36
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO18838 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030044925-A1.
PD 06-MAR-2003.

RESULT 37
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABR78259 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030055474-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 38
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABR39937 standard; protein; 234 AA.
DE Human prostate selective polypeptide Pr340.
PN WO2003014298-A2.
PD 20-FEB-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.

RESULT 39
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABR71958 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

RESULT 40
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABU84995 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030032114-A1.
PD 13-FEB-2003.

RESULT 41
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO00134 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030032101-A1.
PD 13-FEB-2003.

RESULT 42
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO11466 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030036124-A1.
PD 20-FEB-2003.

RESULT 43
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO02111 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030040054-A1.
PD 27-FEB-2003.

RESULT 44
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABU88685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030036133-A1.
PD 20-FEB-2003.

RESULT 45
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABU83380 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030036134-A1.
PD 20-FEB-2003.

RESULT 46
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO06181 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030022294-A1.
PD 30-JAN-2003.

RESULT 47
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABR59217 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030027275-A1.
PD 06-FEB-2003.

RESULT 48
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO09279 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030027324-A1.
PD 06-FEB-2003.

RESULT 49
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO19143 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 50
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO11161 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030036123-A1.
PD 20-FEB-2003.

RESULT 51
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABR66779 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030036148-A1.
PD 20-FEB-2003.

RESULT 52
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO15992 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030040060-A1.
PD 27-FEB-2003.

RESULT 53
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABO13698 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030044916-A1.
PD 06-MAR-2003.

RESULT 54
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
ID ABU71512 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US20030013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.

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Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 55
ID   ABU65601 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein, SEQ ID 66.
PN   US20030036156-A1.
PD   20-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 56
ID   ABO07449 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030032117-A1.
PD   13-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 57
ID   ABO03636 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036128-A1.
PD   06-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 58
ID   ABR67084 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030027266-A1.
PD   06-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 59
ID   ABO15687 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054483-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 60
ID   ABU55968 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein, PRO1864.
PN   US20030022298-A1.
PD   30-JAN-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 61
ID   ABU72293 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20020182638-A1.
PD   05-DEC-2002.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 62
ID   ABU65296 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030032102-A1.
PD   13-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 63
ID   ABU95241 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036117-A1.
PD   20-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 64
ID   ABU71144 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030036143-A1.
PD   20-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;


Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 65
ID   ABO07754 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030032130-A1.
PD   13-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 66
ID   ABR69995 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030032138-A1.
PD   13-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 67
ID   ABR69328 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030036132-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 68
ID   ABO01469 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030008353-A1.
PD   09-JAN-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 69
ID   ABR60068 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030017542-A1.
PD   23-JAN-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 70
ID   ABU81271 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030017542-A1.
PD   23-JAN-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 71
ID   ABR58287 standard; protein; 234 AA.
DE   BCU00092 protein #SEQ ID 20.
PN   WO2003029421-A2.
PD   10-APR-2003.
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 72
ID   ABU90966 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20030018168-A1.
PD   23-JAN-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 73
ID   ABR67803 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030027269-A1.
PD   06-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity 100.0%;            Pred. No. 1.5e-131;

RESULT 74
ID   ABR65191 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864,
PN   US20030027268-A1.
PD   06-FEB-2003.
Query Match           100.0%;  Score 1195;  DB 6;  Length 234;
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Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 75
ID   ABR68413 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030272274-A1.
PD   06-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 76
ID   ABR71825 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030032135-A1.
PD   13-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 77
ID   ABU85305 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030022295-A1.
PA   (GETH) GENENTECH INC.
PD   30-JAN-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 78
ID   ABU88995 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030022297-A1.
PD   30-JAN-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 79
ID   ABU83075 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030032105-A1.
PD   13-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 80
ID   ABU94931 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030032123-A1.
PD   13-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 81
ID   ABU90479 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030032108-A1.
PD   13-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 82
ID   ABU83990 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030032111-A1.
PD   13-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 83
ID   ABU93641 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030032219-A1.
PD   13-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 84
ID   ABR64886 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030027263-A1.
PD   06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 85
ID   ABO27287 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO1864.
PN   US20030009012-A1.
PA   (GETH) GENENTECH INC.
PD   09-JAN-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 86
ID   ABR68718 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030027271-A1.
PD   06-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 87
ID   ABO05534 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036125-A1.
PD   20-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 88
ID   ABR99079 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040068-A1.
PD   27-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 89
ID   ABU56963 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030027280-A1.
PD   06-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 90
ID   ABU85915 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030022300-A1.
PD   30-JAN-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 91
ID   ABU82202 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036136-A1.
PD   20-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 92
ID   ABU87213 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030036138-A1.
PD   20-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 93
ID   ABU83685 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030032109-A1.
PD   13-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 94
ID   ABO08059 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030040066-A1.
PD   27-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 95

ID   ABU92482 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO1864.
PN   US2003045684-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 96
ID   ABU81770 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036157-A1.
PD   20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 97
ID   ABU65934 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003032104-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 98
ID   ABU81152 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864.
PN   US2003036155-A1.
PD   20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 99
ID   ABR59763 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003027212-A1.
PD   06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 100
ID   ABU93951 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032120-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 101
ID   ABU99804 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003022296-A1.
PD   30-JAN-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 102
ID   ABR66474 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864.
PN   US2003027281-A1.
PD   06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 103
ID   ABR90892 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040058-A1.
PD   27-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 104
ID   ABO53267 standard; protein; 234 AA.
DE   Novel human secreted polypeptide PRO1864.
PN   US2003027986-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 105
ID   ABU94319 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003017540-A1.
PD   23-JAN-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 106
ID   ABU79201 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032106-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 107
ID   ABU86530 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein (PRO) #33.
PN   US2003032129-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 108
ID   ABU86835 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032131-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 109
ID   ABU94624 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032107-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 110
ID   ABO04551 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003022301-A1.
PD   30-JAN-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 111
ID   ABR70300 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032139-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 112
ID   ABU98465 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003022301-A1.
PD   30-JAN-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 113
ID   ABR65864 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036165-A1.
PD   20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 114
ID   ABR64581 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027262-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 115
ID   ABU79506 standard; protein; 234 AA.

DE   Human PRO polypeptide #33.
PN   US20030032110-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 116
ID   ABU92897 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036142-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 117
ID   ABU95856 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030036145-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 118
ID   ABU91076 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036154-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 119
ID   ABU90169 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036153-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 120
ID   ABU09584 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030044931-A1.
PD   06-MAR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 121
ID   ABO10856 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036150-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 122
ID   ABR70910 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040069-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 123
ID   ABU98269 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20020183493-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 124
ID   ABU87518 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030022293-A1.
PD   30-JAN-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 125
ID   ABU91386 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030032128-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 126
ID   ABU88274 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036634-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 127
ID   ABU84600 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030032116-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 128
ID   ABR69690 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030032122-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 129
ID   ABU80067 standard; protein; 234 AA.
DE   Human PRO protein #33.
PN   US20030036139-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 130
ID   ABU82481 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20020183494-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 131
ID   ABU93336 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030017541-A1.
PD   23-JAN-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 132
ID   ABO09889 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030017543-A1.
PD   23-JAN-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 133
ID   ABO08974 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036152-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 134
ID   ABU96445 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20030027993-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 135
ID   ABU10542 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein #33.
PN   US2002127584-A1.

```
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;
     Best Local Similarity      100.0%;

RESULT 136
ID   ABU72115 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003023042-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 137
ID   ABU95551 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032115-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 138
ID   ABU96760 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032140-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 139
ID   ABR70605 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040076-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 140
ID   ABO04956 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003008352-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 141
ID   ABO08364 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044922-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 142
ID   ABO05571 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032118-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 143
ID   ABR73960 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 144
ID   ABR95552 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036135-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 145
ID   ABR80849 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 146
ID   ABR81154 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 147
ID   ABM00850 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 148
ID   ABR88452 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054479-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 149
ID   ABM77273 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 150
ID   ABO28757 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 151
ID   ABO31502 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 152
ID   ABM07919 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 153
ID   ABO40399 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match                100.0%;    Score 1195;    DB 6;    Length 234;
     Best Local Similarity      100.0%;    Pred. No. 1.5e-131;

RESULT 154
ID   ABO35824 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
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PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 155
ID   ABO43963 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 156
ID   ADA77818 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 157
ID   ABM24758 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104539-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 158
ID   ABO03026 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036131-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 159
ID   ABR90282 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040075-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 160
ID   ABM17196 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 161
ID   ABR94942 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044930-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 162
ID   ABR95247 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040071-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 163
ID   ADB17071 standard; protein; 234 AA.
DE   Human transmembrane PRO polypeptide (SeqID 14).
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 164
ID   ABO21485 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 165
ID   ABR97749 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 166
ID   ABR87537 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 167
ID   ABM77578 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 168
ID   ABM27808 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064440-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 169
ID   ABM06089 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 170
ID   ABM03595 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 171
ID   ABM35046 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 172
ID   ABM26283 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.5e-131;

RESULT 173
ID   ABO48065 standard; protein; 234 AA.

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DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049749-A1
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 174
ID   ABR92807 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 175
ID   ABO24568 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 176
ID   ABM1579 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 177
ID   ABM02680 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 178
ID   ABM15976 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 179
ID   ABO27537 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 180
ID   ABM29028 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 181
ID   ABM07004 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068699-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 182
ID   ABM21098 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003067707-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 183
ID   ABM09444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 184
ID   ABO41314 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 185
ID   ABO36129 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 186
ID   ABO43658 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 187
ID   ABM76358 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003082717-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 188
ID   ABM76054 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104548-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 189
ID   ABM25673 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104542-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 190
ID   ABM25978 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104543-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 191
ID   ABO03331 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036127-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
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RESULT 192
ID   AB002416 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040061-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 193
ID   AB044245 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO1864.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 194
ID   AB090587 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036130-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 195
ID   ABR73655 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 196
ID   AB016907 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 197
ID   ABR94332 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044917-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 198
ID   ABR75839 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044929-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 199
ID   ABR71215 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059880-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 200
ID   ABR93112 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064465-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 201
ID   ABR93417 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054478-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 202
ID   ABR87842 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068718-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 203
ID   AB027842 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064454-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 204
ID   AB029977 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064461-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 205
ID   AB033186 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068724-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 206
ID   ABM04874 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068727-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 207
ID   ABM08834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068772-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 208
ID   AB036434 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068714-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 209
ID   AB035519 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068758-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 210
ID   AB039484 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068776-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.

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Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 211
ID   ABM10359 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003069407-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 212
ID   ABM11884 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104555-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 213
ID   ABO52030 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049768-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 214
ID   ABO52335 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049771-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 215
ID   ADA19876 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 216
ID   ABO23653 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032134-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 217
ID   ADB17259 standard; protein; 234 AA.
DE   Human transmembrane PRO polypeptide (SeqID 14).
PN   US2003050465-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 218
ID   ABR97139 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 219
ID   ABR86927 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864,
PN   US2003049778-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;

RESULT 220
ID   ABM10969 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 221
ID   ABM28813 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 222
ID   ABO32112 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 223
ID   ABM15239 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 224
ID   ABM06394 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 225
ID   ABM04205 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 226
ID   ABM22318 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 227
ID   ABM07614 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 228
ID   ABO40704 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                      100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 229
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RESULT 230
ID   ABM35351 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200307179-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 231
ID   ABM33114 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200307374-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 232
ID   ABO52640 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US200304973-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 233
ID   ABO50200 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200304977-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 234
ID   ABU99194 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200304055-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 235
ID   ABO04246 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200304164-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 236
ID   ABO05876 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200304074-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 237
ID   ABM18416 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200305985-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 238
ID   ABR97444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200305480-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

ID   ABR80544 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200304974-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 239
ID   ABM01155 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200304770-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 240
ID   ABR88757 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200304957-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 241
ID   ABM13409 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200306457-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 242
ID   ABM20793 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200306711-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 243
ID   ABO41924 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200304745-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 244
ID   ABO42534 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200304751-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 245
ID   ABM10054 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200306478-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 246
ID   ABO38569 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US200306873-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 247
ID   ABM32809 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US200307185-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
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RESULT 248
ID   ABM22623 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030087373-A1.
PD   08-MAY-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 249
ID   ABM74834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030096353-A1.
PD   22-MAY-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 250
ID   ADA79610 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030073173-A1.
PD   17-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 251
ID   ABR96224 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054458-A1.
PD   20-MAR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 252
ID   ABM02375 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030059886-A1.
PD   27-MAR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 253
ID   ABR86317 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049758-A1.
PD   13-MAR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 254
ID   ABR86622 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049772-A1.
PD   13-MAR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 255
ID   ABM16586 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064448-A1.
PD   03-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 256
ID   ABM29638 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064456-A1.
PD   03-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 257
ID   ABO29062 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068693-A1.
PD   10-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 258
ID   ABM23843 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030067735-A1.
PD   10-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 259
ID   ABM23233 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068753-A1.
PD   10-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 260
ID   ABM22013 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068742-A1.
PD   10-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 261
ID   ABO37654 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068756-A1.
PD   10-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 262
ID   ABM28418 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030082715-A1.
PD   01-MAY-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 263
ID   ABM28723 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030082716-A1.
PD   01-MAY-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 264
ID   ABM66367 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068737-A1.
PD   10-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 265
ID   ABM75749 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20031045547-A1.
PD   05-JUN-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;
PA   (GETH) GENENTECH INC.

RESULT 266
ID   ABM34029 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030096359-A1.
PD   22-MAY-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 267
ID   ABM34334 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20031000601-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 268
ID   ABO20265 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030032125-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 269
ID   ABO21180 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054454-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 270
ID   ABO22095 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054477-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 271
ID   ADA20048 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030055222-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 272
ID   ABO34173 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO 1864.
PN   US20030060601-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 273
ID   ABR96529 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054460-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 274
ID   ABR85707 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049753-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 275
ID   ABR99689 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049763-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 276
ID   ABM00545 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073172-A1.
PD   17-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 277
ID   ABM00240 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073172-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 278
ID   ABO29672 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068700-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 279
ID   ABM23538 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068736-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 280
ID   ABM29333 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068679-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 281
ID   ABO38264 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068767-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 282
ID   ABO45564 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030073182-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 283
ID   ABM20488 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104557-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 284
ID   ADA81337 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030092121-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 285
ID   ABO16602 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030027276-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;

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        Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                          Pred. No. 1.5e-131;
ID   ABO18228 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044920-A1.
PD   06-MAR-2003.

RESULT 287
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO22655 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003027265-A1.
PD   06-FEB-2003.

RESULT 288
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO22960 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003054461-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 289
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABR92502 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064446-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 290
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABR81459 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 291
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABM77883 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049783-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 292
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABR89672 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073171-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 293
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABM26588 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032121-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 294
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABM13714 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064458-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 295
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO28452 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064460-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 296
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO30282 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064464-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 297
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABM07309 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068702-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 298
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABM03900 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068734-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 299
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO37044 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068719-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 300
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO41619 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068729-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 301
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO35214 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068738-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 302
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABM25063 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104540-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.

RESULT 303
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO47455 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049742-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 304
Query Match             100.0%;
Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                                  Pred. No. 1.5e-131;
ID   ABO47760 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049747-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
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Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 305
ID AB048370 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 306
ID AB051420 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 307
ID AB051725 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 308
ID AB050505 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO)
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 309
ID ABR79629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 310
ID ABM16891 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 311
ID ABO17923 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 312
ID ABO20875 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 313
ID ABR96834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 314
ID ABM12189 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 315
ID ABM16281 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 316
ID ABM24148 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 317
ID ABM14629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 318
ID ABM04510 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 319
ID ABM06699 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 320
ID ABM09139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 321
ID ABO39179 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 322
ID ABM75444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%;   Pred. No. 1.5e-131;
RESULT 323
ID ABM25568 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104541-A1.
PD 05-JUN-2003.

RESULT 324
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABM19878 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

RESULT 325
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABO46784 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 326
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABO47089 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 327
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ADA83135 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 328
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABR71520 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 329
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABR72130 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 330
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABO06839 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 331
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABR84792 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 332
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABR73350 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 333
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABR76444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 334
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABR73045 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 335
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABM18111 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 336
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABO20570 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 337
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABO25313 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 338
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABO25618 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 339
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABR94027 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 340
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABR79934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 341
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;
ID ABM11274 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 342
Query Match Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
             100.0%; Pred. No. 1.5e-131;

RESULT 343
Query Match Best Local Similarity 100.0%;

ID AB032881 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030644453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
PD 03-APR-2003.

RESULT 344
ID AB030587 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030644466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 345
ID AB030892 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030687760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 346
ID ABM27198 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030688760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 347
ID ABM29943 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030688769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 348
ID ABM05479 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030455700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 349
ID ABM15544 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030688698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 350
ID ABM08529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 351
ID AB042229 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 352
ID AB037959 standard; protein; 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.
PN US20030068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 353
ID ABO45869 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 354
ID ABM66672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068888-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 355
ID ADB20178 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 356
ID ABM19573 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 357
ID ABO49285 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 358
ID ABO49590 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 359
ID ADA78430 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 360
ID ABR88147 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 361
ID ADA00345 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US20030027992-A1.

PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 362
ID   ABM26893 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068739-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 363
ID   ABO39789 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068689-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 364
ID   ABM03290 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049776-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 365
ID   ABO49895 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049780-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 366
ID   ABO50810 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036126-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 367
ID   ABO05266 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044924-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 368
ID   ABR74570 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044927-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 369
ID   ABR77049 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040072-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 370
ID   ABM17806 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040072-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 371

ID   ABR95857 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040073-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 372
ID   ABO21790 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054475-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 373
ID   ABO19960 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032124-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 374
ID   ABO24263 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049759-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 375
ID   ABR86012 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064467-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 376
ID   ABM10664 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064455-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 377
ID   ABM76663 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054465-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 378
ID   ABM93367 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073170-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 379
ID   ABM12494 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073176-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 380
ID   ABM05784 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068717-A1.
PD   10-APR-2003.

RESULT 381
ID   AB034909 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068728-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 382
ID   ABM02985 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 383
ID   ABM18963 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 384
ID   ABM19268 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length~234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 385
ID   ABO46479 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 386
ID   ABO48980 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049757-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 387
ID   ABR69023 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027273-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 388
ID   ABR89062 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036119-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 389
ID   ABR72435 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036120-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 390

RESULT 390
ID   ABR74265 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 391
ID   ABO18533 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044921-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 392
ID   ABR80239 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 393
ID   ABM01460 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 394
ID   ABM02070 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 395
ID   ABR87232 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 396
ID   ABM12799 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 397
ID   ABM30553 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 398
ID   ABM24453 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 399
ID   ABO29367 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.

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PN   US20030068697-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
                                      Length 234;
RESULT 400
ID   AB031197 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 401                            Length 234;
ID   ABM14324 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068686-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 402                            Length 234;
ID   ABM09749 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 403                            Length 234;
ID   ABM38874 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 404                            Length 234;
ID   ABM34639 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030104538-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 405                            Length 234;
ID   ABM51115 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049781-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 406                            Length 234;
ID   ABO03941 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036158-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 407                            Length 234;
ID   ABO10411 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030036151-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 408                            Length 234;
ID   ABR77654 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040067-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
                                      Length 234;
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RESULT 409
ID   ABR78864 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054456-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 410                            Length 234;
ID   ABO23958 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 411                            Length 234;
ID   ABR93722 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 412                            Length 234;
ID   ABM01765 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030059883-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 413                            Length 234;
ID   ABM78188 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 414                            Length 234;
ID   ABR89977 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 415                            Length 234;
ID   ABM27503 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 416                            Length 234;
ID   ABM13104 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 417                            Length 234;
ID   ABO31807 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068731-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;
     Best Local Similarity  100.0%;   Score 1195;  DB 7;
                                      Pred. No. 1.5e-131;
RESULT 418                            Length 234;
ID   ABM14019 standard; protein; 234 AA.
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DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068683-A1.
PD 10-APR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 419
ID ABM08224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068754-A1.
PD 10-APR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 420
ID ABO40094 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030068681-A1.
PD 10-APR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 421
ID ABM74529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030096351-A1.
PD 22-MAY-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 422
ID ABM33724 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030096358-A1.
PD 22-MAY-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 423
ID ABM20183 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030104556-A1.
PD 05-JUN-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 424
ID ABO48675 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030049756-A1.
PD 13-MAR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 425
ID ABR72740 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030103122-A1.
PD 20-FEB-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 426
ID ABO15382 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030036121-A1.
PD 20-FEB-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 427
ID ABR85097 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030040055-A1.
PD 27-FEB-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;

    Best Local Similarity   100.0%;   Pred. No. 1.5e-131;

RESULT 428
ID ABO15077 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030049919-A1.
PD 06-MAR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 429
ID ABM17501 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030044928-A1.
PD 06-MAR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 430
ID ABO17212 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030040077-A1.
PD 27-FEB-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 431
ID ABR85402 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030049746-A1.
PD 13-MAR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 432
ID ABM76968 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054464-A1.
PD 20-MAR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 433
ID ABO28147 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030064459-A1.
PD 03-APR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 434
ID ABM22928 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068757-A1.
PD 10-APR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 435
ID ABM30248 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068723-A1.
PD 10-APR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 436
ID ABM21708 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068741-A1.
PD 10-APR-2003.
    Query Match
    Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                             100.0%;   Pred. No. 1.5e-131;
PA (GETH) GENENTECH INC.

RESULT 437
ID ABM21403 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

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PN   US20030687744-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 438
ID   ABM14934 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030687766-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 439
ID   ABO41009 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030688694-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 440
ID   ABO36739 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030688715-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 441
ID   ABO37349 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030688726-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 442
ID   ABM75139 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20031044544-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 443
ID   ABM33419 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030996357-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 444
ID   ABO46174 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049760-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 445
ID   ADA82501 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049755-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 446
ID   ADB85587 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030049735-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 447
ID   ABM31773 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030688680-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 448
ID   ABM31163 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030688762-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 449
ID   ADB85809 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054472-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 450
ID   ABM32078 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030688708-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 451
ID   ABM32383 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030688713-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 452
ID   ADB68266 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030065161-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 453
ID   ADB68073 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030606600-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 454
ID   ABM31468 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030688761-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score  1195;  DB  7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;
PA   (GETH ) GENENTECH INC.

RESULT 455
ID   ABM30858 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030688771-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 456
ID   ADB90890 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030834473-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

ID   ADC06970 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030060602-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 457
ID   ADC17149 standard; protein; 234 AA.
DE   Mammalian PRO polypeptide (SeqID 14).
PN   US20030065143-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 458
ID   ADC14847 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030073208-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 459
ID   ADC52342 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein (PRO) #33.
PN   US20030138882-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 460
ID   ADD05539 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030087376-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 461
ID   ADD10351 standard; protein; 234 AA.
DE   Novel human secreted/transmembrane PRO polypeptide #31.
PN   US20030105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 462
ID   ADD11311 standard; protein; 234 AA.
DE   Novel human secreted/transmembrane PRO polypeptide #31.
PN   US20030105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 463
ID   ADD37104 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US20030105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 464

Best Local Similarity   100.0%;   Pred. No. 1.5e-131;
RESULT 465
ID   ADD36018 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030105298-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 466
ID   ADG01019 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030078387-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 467
ID   ADG08572 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030180793-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 468
ID   ADG02534 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030207397-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 469
ID   ADG01241 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030207399-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 470
ID   ADF95416 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030207398-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 471
ID   ADF95193 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030207392-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 472
ID   ADG12231 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030180795-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 473
ID   ADH24046 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030180918-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match
Best Local Similarity   100.0%;   Score 1195;   DB 7;   Length 234;
                        100.0%;   Pred. No. 1.5e-131;
RESULT 474
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ID   ADH34072 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180858-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 475
ID   ADH29905 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180859-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 476
ID   ADH23876 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180919-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 477
ID   ADH08891 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003207395-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 478
ID   ADG85280 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180904-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 479
ID   ADH24556 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180907-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 480
ID   ADH37412 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003181646-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 481
ID   ADH02001 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180837-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 482
ID   ADH37582 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003181648-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 483
ID   ADG85620 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180905-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 484
ID   ADH24216 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180914-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 485
ID   ADH38510 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181643-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 486
ID   ADG83631 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180794-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 487
ID   ADH29439 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180860-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 488
ID   ADH27555 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180906-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 489
ID   ADH37752 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003181647-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 490
ID   ADH37929 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003181649-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 491
ID   ADH57349 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180920-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7;   Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 492
ID   ADH53491 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.

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PN  US20031B1636-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;
    Best Local Similarity  100.0%;  Score 1195;  DB 7;  Length 234;
RESULT 493
ID  ADH53661 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1641-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 494
ID  ADH51997 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1638-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 495
ID  ADH49852 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1639-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 496
ID  AD125362 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1696-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 497
ID  ADH90155 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1698-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 498
ID  AD125532 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1669-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 499
ID  ADH97706 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1672-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 500
ID  AD103554 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1656-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 501
ID  AD111911 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US20031B1666-A1.

PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 502
ID  ADH99985 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1697-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 503
ID  ADH98386 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1707-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 504
ID  AD111061 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US20031B1682-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 505
ID  AD111571 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US20031B1684-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 506
ID  ADH98216 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1709-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 507
ID  ADH98556 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1708-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 508
ID  ADH90046 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1673-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 509
ID  AD105034 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B0848-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.5e-131;
RESULT 510
ID  AD103384 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US20031B1654-A1.
PD  25-SEP-2003.
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PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 511
ID ADI04779 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 512
ID ADH78233 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 513
ID ADI19577 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 514
ID ADH90325 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 515
ID ADI03044 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 516
ID ADH77893 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 517
ID ADH97876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 518
ID ADI01261 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 519
ID ADI01956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 520
ID ADIO3214 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 521
ID ADI11401 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 522
ID ADIO2303 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 523
ID ADI11741 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 524
ID ADI05378 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 525
ID ADH79450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 526
ID ADI19407 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 527
ID ADI05208 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 528
ID ADH79620 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191288-A1.
PD 09-OCT-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;

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Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 529
ID   ADI01446 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031681678-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 530
ID   ADI01616 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031681680-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 531
ID   ADI01786 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031681679-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 532
ID   ADH79790 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031691289-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 533
ID   ADI04608 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031711550-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 534
ID   ADI02744 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031811551-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 535
ID   ADH78063 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20031811677-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 536
ID   ADI25702 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031811670-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 537
ID   ADI25872 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031811671-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;


RESULT 538
ID   ADK65384 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031073821-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 539
ID   ADH98726 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031191284-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 540
ID   ADH79967 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031191287-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 541
ID   ADL32672 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031207396-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 542
ID   ADM30206 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031073813-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 543
ID   ADL93698 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031040013-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 544
ID   ADC52152 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031130483-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 7;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 545
ID   ADE41312 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US20031100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 8;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 546
ID   ADE74203 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20032211572-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match    100.0%;    Score 1195;   DB 8;   Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.5e-131;

RESULT 547
ID   ADE74815 standard; protein; 234 AA.
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DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003211574-A1.
PD   13-NOV-2003.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 548
ID   ADF96028 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003215909-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.

RESULT 549
ID   ADG04299 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003215912-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 550
ID   ADG00459 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003215911-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 551
ID   ADG06584 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180853-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 552
ID   ADH06414 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180855-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 553
ID   ADG68835 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180912-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 554
ID   ADH27725 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180913-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 555
ID   ADH25066 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003166848-A1.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 556
ID   ADH33698 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181645-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 557
ID   ADG82715 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003215910-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.

RESULT 558
ID   ADH02341 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180839-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 559
ID   ADH07948 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180845-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 560
ID   ADG69345 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180846-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 561
ID   ADH39166 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180917-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 562
ID   ADH25996 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003068770-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 563
ID   ADG83906 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180842-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match           100.0%;    Score 1195;    DB 8;    Length 234;
Best Local Similarity 100.0%;    Pred. No. 1.5e-131;

RESULT 564
ID   ADG85450 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003166848-A1.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.

RESULT 565
ID   ADH06244 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180854-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
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Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 566
ID ADH30074 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 567
ID ADH24386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 568
ID ADH32965 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 569
ID ADG69515 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 570
ID ADH07778 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 571
ID ADG85790 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 572
ID ADH39336 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 573
ID ADH33528 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 574
ID ADH33868 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 575
ID ADH01078 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 576
ID ADG69685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 577
ID ADH02171 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 578
ID ADG69175 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 579
ID ADG85960 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 580
ID ADH24896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 581
ID ADH39513 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 582
ID ADH02511 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 583
ID ADG69005 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 584
ID ADH07608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 585
ID ADG86130 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 586
ID ADH24726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 587
ID ADH25774 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 588
ID ADH38340 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 589
ID ADH57179 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 590
ID ADH43495 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 591
ID ADH52167 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 592
ID ADH49533 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 593

ID ADH90495 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 594
ID ADI11231 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 595
ID ADH98896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 596
ID ADI02126 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 597
ID ADH90665 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 598
ID ADJ54704 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 599
ID ADJ98540 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 600
ID ADJ98710 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 601
ID ADH78869 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 602
ID ADJ99103 standard; protein; 234 AA.

DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318640B-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 603
ID   ADJ99273 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318196-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 604
ID   ADJ98891 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318724Z-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 605
ID   ADH79039 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318170Z-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 606
ID   ADK00899 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US200318607-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 607
ID   ADK14420 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200318729-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 608
ID   ADK82840 standard; protein; 234 AA.
DE   Human PRO polypeptide #31.
PN   US200403837-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 609
ID   ADJ64475 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US200408337-A1.
PD   04-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 610
ID   ADM31371 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200404334-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 611
ID   ADM36418 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.

PN   US200405335B-A1.
PD   18-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 612
ID   ADM40223 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200404835B-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 613
ID   ADM80869 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US200405841I-A1.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 614
ID   ADL91873 standard; protein; 234 AA.
DE   Human PRO1864 protein SEQ ID NO:94.
PN   WO200402407G-A2.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 615
ID   ADN37831 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US200409195Y-A1.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 616
ID   ADY18016 standard; protein; 234 AA.
DE   PRO polypeptide SEQ ID NO 3822.
PN   WO200501696Z-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 9; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 617
ID   ADY19397 standard; protein; 234 AA.
DE   PRO polypeptide SEQ ID NO 5203.
PN   WO200501696Z-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 9; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 618
ID   ADY77109 standard; protein; 234 AA.
DE   Neoplastic disease detection protein PRO1864.
PN   US200505910Z-A1.
PD   17-MAR-2005.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD P J.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
Query Match   100.0%; Score 1195; DB 9; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.5e-131;

RESULT 619
ID   AEA08359 standard; protein; 234 AA.
DE   Steriodogenic acute regulatory protein related (MLN64).
PN   WO200504753G-A2.

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PD   26-MAY-2005.
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
     Query Match             100.0%;  Score 1195;  DB 9;   Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.5e-131;

RESULT 620
ID   AAM41716 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 6647.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             100.0%;  Score 1195;  DB 4;   Length 238;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 621
ID   AAM41715 standard; protein; 238 AA.
DE   Human secretory polypeptide SEQ ID NO 6646.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match             100.0%;  Score 1195;  DB 6;   Length 238;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 622
ID   ABP75508 standard; protein; 238 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 692.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match             100.0%;  Score 1195;  DB 6;   Length 238;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 623
ID   ABR58404 standard; protein; 234 AA.
DE   Human NOV19b
PN   WO200329423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match             99.6%;   Score 1188;  DB 6;   Length 234;
     Best Local Similarity   99.4%;   Pred. No. 1e-130;

RESULT 624
ID   AAM39930 standard; protein; 216 AA.
DE   Human polypeptide SEQ ID NO 3075.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             91.8%;   Score 1097;  DB 5;   Length 216;
     Best Local Similarity   92.3%;   Pred. No. 4.7e-120;

RESULT 625
ID   ABB90287 standard; protein; 201 AA.
DE   Human polypeptide SEQ ID NO 2663.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             85.7%;   Score 1024;  DB 5;   Length 201;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-111;

RESULT 626
ID   ABR58403 standard; protein; 198 AA.
DE   Human NOV19a
PN   WO200302423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match             82.4%;   Score 985;   DB 6;   Length 198;
     Best Local Similarity   84.6%;   Pred. No. 6.2e-107;

RESULT 627
ID   AAU30250 standard; protein; 283 AA.
DE   Novel human secreted protein #741.
PN   WO200179449-A2.
PD   25-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             65.0%;   Score 777;   DB 4;   Length 283;
     Best Local Similarity   72.5%;   Pred. No. 3e-82;

RESULT 628
ID   ADB64413 standard; protein; 176 AA.
DE   Human protein encoded by clone FEBRA20007820.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match             56.0%;   Score 669.5; DB 7;   Length 176;
     Best Local Similarity   87.5%;   Pred. No. 6.9e-70;

RESULT 629
ID   ADK36828 standard; protein; 146 AA.
DE   Novel human polypeptide SeqID8910.
PN   WO200216439-A2.
PD   28-FEB-2002.
PA   (HYSE-) HYSEQ INC.
     Query Match             55.6%;   Score 665;   DB 9;   Length 146;
     Best Local Similarity   91.0%;   Pred. No. 1.8e-69;

RESULT 630
ID   ADZ88813 standard; protein; 383 AA.
DE   Breast specific protein SEQ ID NO 180.
PN   WO200504075-A2.
PD   19-MAY-2005.
PA   (DIAD-) DIADEXUS INC.
     Query Match             55.6%;   Score 664;   DB 9;   Length 383;
     Best Local Similarity   56.2%;   Pred. No. 9e-69;

RESULT 631
ID   AAW25768 standard; protein; 445 AA.
DE   Human MLN 64.
PN   WO9706256-A2.
PD   20-FEB-1997.
PA   (INRM-) INST NAT SANTE & RECH MEDICALE.
PA   (CNRS-) CENT NAT RECH SCI.
PA   (UYPA-) UNIV PASTEUR LOUIS.
PA   (BRIM-) BRISTOL-MYERS SQUIBB CO.
     Query Match             55.6%;   Score 664;   DB 2;   Length 445;
     Best Local Similarity   56.2%;   Pred. No. 1.1e-68;

RESULT 632
ID   ABR47530 standard; protein; 445 AA.
DE   Breast cancer associated protein sequence SEQ ID NO:296.
PN   WO200304989-A2.
PD   16-JAN-2003.
PA   (MILL-) MILLENIUM PHARM INC.
     Query Match             55.6%;   Score 664;   DB 6;   Length 445;
     Best Local Similarity   56.2%;   Pred. No. 1.1e-68;

RESULT 633
ID   ADH12184 standard; protein; 445 AA.
DE   Human polypeptide #7.
PN   WO200504534-A2.
PD   26-MAY-2005.
PA   (HYSE-) HYSEQ INC.
     Query Match             55.6%;   Score 664;   DB 8;   Length 445;
     Best Local Similarity   56.2%;   Pred. No. 1.1e-68;

RESULT 634
ID   AEA15071 standard; protein; 445 AA.
DE   Human malignant neoplasia-related protein SeqID33.
PN   EP1365034-A2.
PD   26-NOV-2003.
PA   (FARB ) BAYER AG.
     Query Match             55.6%;   Score 664;   DB 8;   Length 445;
     Best Local Similarity   56.2%;   Pred. No. 1.1e-68;

RESULT 635
ID   ADZ88812 standard; protein; 497 AA.
DE   Breast specific protein SEQ ID NO 179.
PN   WO200504075-A2.
PD   19-MAY-2005.
PA   (DIAD-) DIADEXUS INC.
     Query Match             55.6%;   Score 664;   DB 9;   Length 497;
     Best Local Similarity   56.2%;   Pred. No. 1.3e-68;

RESULT 636
ID   ABG05498 standard; protein; 534 AA.
DE   Novel human diagnostic protein #5489.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             52.3%;   Score 625;   DB 4;   Length 534;
     Best Local Similarity   48.9%;   Pred. No. 5.5e-64;

RESULT 637
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ID ABR69622 standard; protein; 412 AA.
DE Human CGDD-22 protein.
PN WO200302726 3-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
RESULT 638
Query Match 48.4%; Score 578; DB 6; Length 412;
Best Local Similarity 58.3%; Pred. No. 1.3e-58;

ID ABP75900 standard; protein; 111 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1084.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
RESULT 639
Query Match 33.9%; Score 405.5; DB 6; Length 111;
Best Local Similarity 73.7%; Pred. No. 9.2e-31;

ID ABB59968 standard; protein; 580 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6696.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
RESULT 640
Query Match 28.7%; Score 343; DB 4; Length 580;
Best Local Similarity 37.8%; Pred. No. 9.2e-31;

ID AAM90384 standard; protein; 70 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:17977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 641
Query Match 26.9%; Score 322; DB 4; Length 70;
Best Local Similarity 98.4%; Pred. No. 1.5e-29;

ID AAB96837 standard; protein; 424 AA.
DE Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
RESULT 642
Query Match 21.9%; Score 93.5; DB 4; Length 424;
Best Local Similarity 7.8%; Pred. No. 0.13;

ID AAU03699 standard; protein; 373 AA.
DE Group B Streptococcus antigenic protein ID-176.
PN WO200132882-A2.
PD 10-MAY-2001.
PA (MICR-) MICROBIAL TECHNICS LTD.
RESULT 643
Query Match 25.7%; Score 91; DB 8; Length 373;
Best Local Similarity 7.8%; Pred. No. 0.22;

ID ADV89705 standard; protein; 605 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 2099.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
(CNRS) CNRS CENT NAT RECH SCI.
RESULT 644
Query Match 25.7%; Score 91; DB 8; Length 605;
Best Local Similarity 7.6%; Pred. No. 0.43;

ID ADV80958 standard; protein; 605 AA.
DE Streptococcus agalactiae protein, SEQ ID 2099.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
(CNRS) CNRS CENT NAT RECH SCI.
RESULT 645
Query Match 25.7%; Score 91; DB 8; Length 605;
Best Local Similarity 7.6%; Pred. No. 0.43;

ID ABP30317 standard; protein; 651 AA.
DE Streptococcus polypeptide SEQ ID NO 9810.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.

Query Match 25.7%; Score 91; DB 5; Length 651;
Best Local Similarity 7.6%; Pred. No. 0.48;
RESULT 646
ID ADV83104 standard; protein; 651 AA.
DE Streptococcus agalactiae protein, SEQ ID 4245.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
(CNRS) CNRS CENT NAT RECH SCI.
RESULT 647
Query Match 25.7%; Score 91; DB 8; Length 651;
Best Local Similarity 7.6%; Pred. No. 0.48;
ID ABP29732 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 8640.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
RESULT 648
Query Match 25.7%; Score 91; DB 5; Length 654;
Best Local Similarity 7.6%; Pred. No. 0.48;
ID ABP26469 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 2114.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
RESULT 649
Query Match 25.7%; Score 91; DB 5; Length 654;
Best Local Similarity 7.6%; Pred. No. 0.48;
ID AAG61678 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.
PN EP1033405-A2.
PD 06-SEP-2000.
RESULT 650
Query Match 21.4%; Score 87.5; DB 3; Length 155;
Best Local Similarity 7.3%; Pred. No. 0.17;
ID AAG59838 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
PN EP1033405-A2.
PD 06-SEP-2000.
RESULT 651
Query Match 21.4%; Score 87.5; DB 3; Length 155;
Best Local Similarity 7.3%; Pred. No. 0.17;
ID AAB59945 standard; protein; 516 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 652
Query Match 25.2%; Score 87.5; DB 3; Length 516;
Best Local Similarity 7.3%; Pred. No. 0.9;
ID ADQ39266 standard; protein; 421 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 929.
PN WO200405805 2-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
RESULT 653
Query Match 23.7%; Score 87; DB 8; Length 421;
Best Local Similarity 7.3%; Pred. No. 0.77;
ID ADQ39263 standard; protein; 223 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 926.
PN WO200405805 2-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
RESULT 654
Query Match 25.5%; Score 85.5; DB 8; Length 223;
Best Local Similarity 7.2%; Pred. No. 0.48;
ID ADQ39258 standard; protein; 285 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 921.
PN WO200405805 2-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.

RESULT 655
ID ADQ39262 standard; protein; 315 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 925.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 8; Length 315; Pred. No. 0.68;

RESULT 656
ID ADQ39260 standard; protein; 323 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 923.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 8; Length 323; Pred. No. 0.78;

RESULT 657
ID ADQ39261 standard; protein; 328 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 924.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 8; Length 328; Pred. No. 0.8;

RESULT 658
ID ADQ39265 standard; protein; 338 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 928.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 8; Length 338; Pred. No. 0.82;

RESULT 659
ID ADQ39267 standard; protein; 339 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 930.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 8; Length 339; Pred. No. 0.86;

RESULT 660
ID ADE28099 standard; protein; 340 AA.
DE Human NTRAN protein - SEQ ID 4.
PN WO2003051902-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 7; Length 340; Pred. No. 0.86;

RESULT 661
ID ADQ39269 standard; protein; 384 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 932.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 8; Length 384; Pred. No. 0.86;

RESULT 662
ID ADQ39264 standard; protein; 390 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 927.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 8; Length 390; Pred. No. 0.86;

RESULT 663
ID ABU26680 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #12207.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match   25.5%;
Best Local Similarity   7.2%;   Score 85.5; DB 6; Length 396; Pred. No. 1;

RESULT 664
ID AAW13575 standard; protein; 438 AA.
DE Batten disease polypeptide CLN3.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match   24.8%;
Best Local Similarity 21.0%;   Score 85.5; DB 2; Length 438; Pred. No. 1.1;

RESULT 665
ID AAW13589 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match   24.8%;
Best Local Similarity 25.5%;   Score 85.5; DB 2; Length 438; Pred. No. 1.2;

RESULT 666
ID AAW13582 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L204.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match   24.8%;
Best Local Similarity 25.5%;   Score 85.5; DB 2; Length 438; Pred. No. 1.2;

RESULT 667
ID AAW13577 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L46.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match   24.8%;
Best Local Similarity 25.5%;   Score 85.5; DB 2; Length 438; Pred. No. 1.2;

RESULT 668
ID ADQ96392 standard; protein; 438 AA.
DE T cell activation associated protein #285.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (ASAHI-) ASAHI KASEI PHARMA CORP.
Query Match   24.8%;
Best Local Similarity 25.5%;   Score 85.5; DB 2; Length 438; Pred. No. 1.2;

RESULT 669
ID ADQ39268 standard; protein; 438 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 931.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   24.8%;
Best Local Similarity 25.5%;   Score 85.5; DB 8; Length 438; Pred. No. 1.2;

RESULT 670
ID ADA05822 standard; protein; 440 AA.
DE Human NOV43a protein SEQ ID NO:182.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match   25.2%;
Best Local Similarity 25.2%;   Score 85.5; DB 8; Length 440; Pred. No. 1.2;

RESULT 671
ID ADN63244 standard; protein; 440 AA.
DE Human NOV43a variant.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
Query Match   25.2%;
Best Local Similarity 25.2%;   Score 85.5; DB 6; Length 440; Pred. No. 1.2;

PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
PD Query Match
PA Best Local Similarity 7.2%; Score 85.5; DB 8; Length 440;

RESULT 672
ID ADN62985 standard; protein; 440 AA.
DE Human NOV43a.
PN US20040038223-A1.
PD 26-FEB-2004.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (GUOX/) GUO X.
PA (LILL/) LI L.
PA (JUUJ/) JU J.
PA (KEKU/) KEKUDA R.
PA (PEYM/) PEYMAN J A.
PA (MILL/) MILLET I.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match
Best Local Similarity 25.2%; Score 85.5; DB 8; Length 440; Pred. No. 1.2;

RESULT 673
ID AAW1593 standard; protein; 467 AA.
DE Batten disease CLN3 mutant protein in family L61.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match
Best Local Similarity 25.5%; Score 85.5; DB 2; Length 467;

RESULT 674
ID ABB89640 standard; protein; 473 AA.
DE Human polypeptide SEQ ID NO 2016.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 25.2%; Score 85.5; DB 5; Length 473; Pred. No. 1.4;

RESULT 675
ID ADQ18055 standard; protein; 473 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN WO200404938-A2.
PD 10-JUN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 473; Pred. No. 1.4;

RESULT 676
ID ADU06406 standard; protein; 473 AA.
DE Novel bronchial cancer-associated human protein SeqID630.
PN DE103167011-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match
Best Local Similarity 25.2%; Score 85.5; DB 9; Length 473; Pred. No. 1.4;

RESULT 677
ID ADY20253 standard; protein; 473 AA.
DE PRO polypeptide SEQ ID NO 6059.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 473; Pred. No. 1.5;

RESULT 678
ID ABU40544 standard; protein; 500 AA.
DE Protein encoded by Prokaryotic essential gene #26071.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 26.0%; Score 85.5; DB 6; Length 500; Pred. No. 1.5;

RESULT 679
ID ADY09432 standard; protein; 527 AA.
DE Plant full length insert polypeptide seqid 65247.
PN US20040034888-A1.
PD 19-FEB-2004.
PA (JIWW/) JI W.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 17.6%; Score 85; DB 8; Length 527; Pred. No. 1.6;

RESULT 680
ID ABU33210 standard; protein; 430 AA.
DE Protein encoded by Prokaryotic essential gene #18737.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 7.1%; Score 84.5; DB 6; Length 430;

RESULT 681
ID AAW13588 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L10.
PN WO9708308-A1.

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PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
RESULT 682
          Query Match             7.1%;  Score  84.5;  DB 2;  Length 322;
          Best Local Similarity  24.8%;  Pred. No. 1.6;
ID   AAG16921 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (HYSE-) HYSEQ INC.
RESULT 683
          Query Match             7.0%;  Score  83.5;  DB 3;  Length 472;
          Best Local Similarity  33.7%;  Pred. No. 1.4;
ID   ABG221285 standard; protein; 472 AA.
DE   Novel human diagnostic protein #21276.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 684
          Query Match             7.0%;  Score  83.5;  DB 4;  Length 239;
          Best Local Similarity  20.1%;  Pred. No. 2.3;
ID   ABU35608 standard; protein; 239 AA.
DE   Protein encoded by Prokaryotic essential gene #21135.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (UYNC-) UNIV NORTH CAROLINA STATE.
RESULT 685
          Query Match             6.9%;  Score  82.5;  DB 6;  Length 389;
          Best Local Similarity  21.7%;  Pred. No. 1.2;
ID   ADU25550 standard; protein; 389 AA.
DE   L. acidophilus cell surface protein homologue #63.
PN   WO2004096992-A2.
PD   11-NOV-2004.
RESULT 686
          Query Match             6.9%;  Score  82.5;  DB 2;  Length 438;
          Best Local Similarity  24.8%;  Pred. No. 2.8;
ID   AAW13590 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L216.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
RESULT 687
          Query Match             6.9%;  Score  82;    DB 7;  Length 589;
          Best Local Similarity  19.5%;  Pred. No. 4.8;
ID   ADB85263 standard; protein; 589 AA.
DE   Mouse RNAi homologue SEQ ID NO:144.
PN   EP1284297-A2.
PD   19-FEB-2003.
PA   (WARN ) WARNER LAMBERT CO.
RESULT 688
          Query Match             6.9%;  Score  81.5;  DB 8;  Length 264;
          Best Local Similarity  33.3%;  Pred. No. 1.8;
ID   ADX74800 standard; protein; 264 AA.
DE   Plant full length insert polypeptide seqid 44166.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
RESULT 689
          Query Match             6.8%;  Score  81.5;  DB 8;  Length 438;
          Best Local Similarity  33.3%;  Pred. No. 1.8;
ID   AAW13586 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L285.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.

RESULT 690
          Query Match             6.8%;  Score  81.5;  DB 2;  Length 519;
          Best Local Similarity  24.8%;  Pred. No. 3.6;
ID   AAB92924 standard; protein; 519 AA.
DE   Human protein sequence SEQ ID NO:11574.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
RESULT 691
          Query Match             6.8%;  Score  81.5;  DB 4;  Length 577;
          Best Local Similarity  22.6%;  Pred. No. 4.6;
ID   ADE28193 standard; protein; 577 AA.
DE   Human MDDT protein - SEQ ID 43.
PN   WO2003046152-A2.
PD   05-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
RESULT 692
          Query Match             6.8%;  Score  81.5;  DB 7;  Length 577;
          Best Local Similarity  22.6%;  Pred. No. 5.3;
ID   ADN23155 standard; protein; 529 AA.
DE   Bacterial polypeptide #5808.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAO/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
RESULT 693
          Query Match             6.8%;  Score  81;    DB 8;  Length 529;
          Best Local Similarity  23.1%;  Pred. No. 5.4;
ID   ADN23156 standard; protein; 529 AA.
DE   Bacterial polypeptide #5809.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAO/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
RESULT 694
          Query Match             6.8%;  Score  81;    DB 8;  Length 529;
          Best Local Similarity  23.1%;  Pred. No. 5.4;
ID   AAG53771 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68491.
PN   EP103405-A2.
PD   06-SEP-2000.
RESULT 695
          Query Match             6.7%;  Score  80.5;  DB 3;  Length 322;
          Best Local Similarity  32.7%;  Pred. No. 3.1;
ID   AAG25639 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 29783.
PN   EP103405-A2.
PD   06-SEP-2000.
RESULT 696
          Query Match             6.7%;  Score  80.5;  DB 3;  Length 322;
          Best Local Similarity  32.7%;  Pred. No. 3.1;
ID   AAG53746 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68457.
PN   EP103405-A2.
PD   06-SEP-2000.
RESULT 697
          Query Match             6.7%;  Score  80.5;  DB 3;  Length 322;
          Best Local Similarity  32.7%;  Pred. No. 3.1;
ID   AB063194 standard; protein; 350 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9711.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
RESULT 698
          Query Match             6.7%;  Score  80.5;  DB 7;  Length 350;
          Best Local Similarity  31.8%;  Pred. No. 3.5;
ID   ABB48552 standard; protein; 463 AA.
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DE   Listeria monocytogenes protein #1256.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
      Query Match   6.7%; Score 80.5; DB 5; Length 463;
      Best Local Similarity   19.0%; Pred. No. 5.1;

RESULT 699
ID   ABU33036 standard; protein; 463 AA.
DE   Protein encoded by Prokaryotic essential gene #18563.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   6.7%; Score 80.5; DB 6; Length 463;
      Best Local Similarity   19.0%; Pred. No. 5.1;

RESULT 700
ID   ADD43870 standard; protein; 536 AA.
DE   Chlamydia trachomatis immunogenic protein, SEQ ID No 165.
PN   WO200304976-A2.
PD   19-JUN-2003.
PA   (CHIR-) CHIRON SPA.
      Query Match   6.7%; Score 80.5; DB 7; Length 536;
      Best Local Similarity   25.2%; Pred. No. 6.3;

RESULT 701
ID   AEA19162 standard; protein; 536 AA.
DE   Chlamydia trachomatis protein - SEQ ID 165.
PN   US2005106162-A1.
PD   19-MAY-2005.
PA   (GRAN/) GRANDI G.
PA   (RATI/) RATTI G.
      Query Match   6.7%; Score 80.5; DB 9; Length 536;
      Best Local Similarity   25.2%; Pred. No. 6.3;

RESULT 702
ID   ADC42920 standard; protein; 891 AA.
DE   Vaccinia Virus Major Core protein P4a precursor.
PN   WO2003017943-A2.
PD   06-MAR-2003.
PA   (MYRI-) MYRIAD GENETICS INC.
      Query Match   6.7%; Score 80.5; DB 7; Length 891;
      Best Local Similarity   23.3%; Pred. No. 13;

RESULT 703
ID   ABB92830 standard; protein; 1780 AA.
DE   Herbicidally active polypeptide SEQ ID NO 2041.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB) BAYER AG.
      Query Match   6.7%; Score 80.5; DB 5; Length 1780;
      Best Local Similarity   20.8%; Pred. No. 33;

RESULT 704
ID   AAB54399 standard; protein; 144 AA.
DE   Human pancreatic cancer antigen protein sequence SEQ ID NO:851.
PN   WO200055320-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match   6.7%; Score 80.5; DB 4; Length 144;
      Best Local Similarity   22.5%; Pred. No. 2.3;

RESULT 705
ID   AAM39952 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 3097.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
      Query Match   6.7%; Score 80.5; DB 3; Length 238;
      Best Local Similarity   25.4%; Pred. No. 1.2;

RESULT 706
ID   ADM04473 standard; protein; 238 AA.
DE   Human protein of the invention SEQ ID NO:3158.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
      Query Match   6.7%; Score 80; DB 7; Length 238;
      Best Local Similarity   22.5%; Pred. No. 2.3;

RESULT 707
ID   AAM41738 standard; protein; 249 AA.

DE   Human polypeptide SEQ ID NO 6669.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
      Query Match   6.7%; Score 80; DB 4; Length 249;
      Best Local Similarity   22.5%; Pred. No. 2.5;

RESULT 708
ID   AAR77844 standard; protein; 309 AA.
DE   Molasses toxicity resistance protein RTM1.
PN   WO9514774-A2.
PD   01-JUN-1995.
PA   (CNRS) CENT NAT RECH SCI.
      Query Match   6.7%; Score 80; DB 2; Length 309;
      Best Local Similarity   28.0%; Pred. No. 3.4;

RESULT 709
ID   ABM67388 standard; protein; 330 AA.
DE   Photorhabdus luminescens protein sequence #485.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
      Query Match   6.7%; Score 80; DB 6; Length 330;
      Best Local Similarity   24.6%; Pred. No. 3.7;

RESULT 710
ID   AAE03831 standard; protein; 360 AA.
DE   Human gene 14 encoded secreted protein HDQFN31, SEQ ID NO: 77.
PN   WO200136440-A1.
PD   25-MAY-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match   6.7%; Score 80; DB 4; Length 360;
      Best Local Similarity   22.5%; Pred. No. 4.1;

RESULT 711
ID   ABG64559 standard; protein; 360 AA.
DE   Human albumin fusion protein
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match   6.7%; Score 80; DB 5; Length 360;
      Best Local Similarity   22.5%; Pred. No. 4.1;

RESULT 712
ID   ADL77826 standard; protein; 360 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1308.
PN   US200401013-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
      Query Match   6.7%; Score 80; DB 8; Length 360;
      Best Local Similarity   22.5%; Pred. No. 4.1;

RESULT 713
ID   ADX62260 standard; protein; 516 AA.
DE   Plant full length insert polypeptide seqid 37103.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
      Query Match   6.7%; Score 80; DB 8; Length 516;
      Best Local Similarity   20.0%; Pred. No. 6.8;

RESULT 714
ID   ABU25554 standard; protein; 365 AA.
DE   Protein encoded by Prokaryotic essential gene #11081.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   6.7%; Score 79.5; DB 6; Length 365;
      Best Local Similarity   21.2%; Pred. No. 4.8;

RESULT 715
ID   AAR58703 standard; protein; 406 AA.
DE   HCMV IB-exon-4 subunit.
PN   WO9417810-A1.

PD   18-AUG-1994.
PA   (WIST-) WISTAR INST ANATOMY & BIOLOGY.
     Query Match   6.7%; Score   79.5; DB   2; Length 406;
     Best Local Similarity   19.3%; Pred. No. 5.6;
RESULT 716
ID   AAW27275 standard; protein; 406 AA.
DE   Human cytomegalovirus immediate-early exon 4 product.
PN   WO9740165-A1.
PD   30-OCT-1997.
PA   (WIST-) WISTAR INST ANATOMY & BIOLOGY.
     Query Match   6.7%; Score   79.5; DB   2; Length 406;
     Best Local Similarity   19.3%; Pred. No. 5.6;
RESULT 717
ID   ABB58483 standard; protein; 638 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 2241.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.7%; Score   79.5; DB   4; Length 638;
     Best Local Similarity   20.5%; Pred. No. 10;
RESULT 718
ID   AAE13277 standard; protein; 723 AA.
DE   Human transporters and ion channels (TRICH)-4.
PN   WO20017174-A2.
PD   18-OCT-2001.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   6.7%; Score   79.5; DB   5; Length 723;
     Best Local Similarity   18.0%; Pred. No. 12;
RESULT 719
ID   ADL12774 standard; protein; 723 AA.
DE   Human steroid-induced C3A liver cell protein #80.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
     Query Match   6.7%; Score   79.5; DB   8; Length 723;
     Best Local Similarity   18.0%; Pred. No. 12;
RESULT 720
ID   AAW20696 standard; protein; 121 AA.
DE   H. pylori secreted or periplasmic protein 05ae20220orf50.
PN   WO9640093-A1.
PD   19-DEC-1996.
PA   (ASTR) ASTRA AB.
     Query Match   6.6%; Score   79; DB   2; Length 121;
     Best Local Similarity   21.4%; Pred. No. 1.2;
RESULT 721
ID   ABB60462 standard; protein; 323 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 8178.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.6%; Score   79; DB   4; Length 323;
     Best Local Similarity   18.8%; Pred. No. 4.7;
RESULT 722
ID   AEB41478 standard; protein; 356 AA.
DE   L. pneumophila protein SEQ ID NO 5810.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   6.6%; Score   79; DB   9; Length 356;
     Best Local Similarity   23.0%; Pred. No. 5.4;
RESULT 723
ID   AEB38189 standard; protein; 358 AA.
DE   L. pneumophila protein SEQ ID NO 2521.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   6.6%; Score   79; DB   9; Length 358;

     Best Local Similarity   23.0%; Pred. No. 5.4;
RESULT 724
ID   ABR58610 standard; protein; 1531 AA.
DE   Human cancer related protein SEQ ID NO:267.
PN   WO2003025138-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match   6.6%; Score   79; DB   6; Length 1531;
     Best Local Similarity   24.3%; Pred. No. 40;
RESULT 725
ID   ADB31753 standard; protein; 1531 AA.
DE   Human 59950 protein #SEQ ID 110.
PN   WO2003065984-A2.
PD   14-AUG-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   6.6%; Score   79; DB   7; Length 1531;
     Best Local Similarity   24.3%; Pred. No. 40;
RESULT 726
ID   ABU62069 standard; protein; 1597 AA.
DE   Human heart alpha-kinase (HK).
PN   US2002177205-A1.
PD   28-NOV-2002.
PA   (RYAZ/) RYAZANOV A.
     Query Match   6.6%; Score   79; DB   6; Length 1597;
     Best Local Similarity   24.3%; Pred. No. 43;
RESULT 727
ID   ABU62070 standard; protein; 1597 AA.
DE   Mouse heart alpha-kinase (HK).
PN   US2002177205-A1.
PD   28-NOV-2002.
PA   (RYAZ/) RYAZANOV A.
     Query Match   6.6%; Score   79; DB   6; Length 1597;
     Best Local Similarity   24.3%; Pred. No. 43;
RESULT 728
ID   ABO55689 standard; protein; 135 AA.
DE   Human genome derived single exon protein #1923.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
     Query Match   6.6%; Score   78.5; DB   8; Length 135;
     Best Local Similarity   59.4%; Pred. No. 1.6;
RESULT 729
ID   ADU02890 standard; protein; 165 AA.
DE   Novel human polypeptide seqid 1357.
PN   WO2004093804-A2.
PD   04-NOV-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
     Query Match   6.6%; Score   78.5; DB   8; Length 165;
     Best Local Similarity   24.6%; Pred. No. 2.1;
RESULT 730
ID   AEB38367 standard; protein; 205 AA.
DE   L. pneumophila protein SEQ ID NO 2699.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   6.6%; Score   78.5; DB   9; Length 205;
     Best Local Similarity   18.3%; Pred. No. 2.9;
RESULT 731
ID   ADB10816 standard; protein; 228 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:4244.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP-) WYETH HOLDINGS CORP.
     Query Match   6.6%; Score   78.5; DB   6; Length 228;
     Best Local Similarity   22.5%; Pred. No. 3.3;
RESULT 732
ID   ABU36298 standard; protein; 239 AA.
DE   Protein encoded by Prokaryotic essential gene #21825.

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PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELITT-) ELITRA PHARM INC.
     Query Match              6.6%;
     Best Local Similarity   23.4%;   Score 78.5;   DB 6;   Pred. No. 3,5;   Length 239;

RESULT 733
ID   ADJ27174 standard; protein; 626 AA.
DE   Human TRICH-6, SEQ ID 6.
PN   WO200401293-A2.
PD   12-FEB-2004.
PA   (INCY-) INCYTE CORP.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 8;   Pred. No. 13;   Length 626;

RESULT 734
ID   ABM84879 standard; protein; 648 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5128.
PN   WO200423973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 8;   Pred. No. 14;   Length 648;

RESULT 735
ID   ABM84877 standard; protein; 668 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5126.
PN   WO200423973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 8;   Pred. No. 15;   Length 668;

RESULT 736
ID   ABP29904 standard; protein; 669 AA.
DE   Streptococcus polypeptide SEQ ID NO 8984.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match              6.6%;
     Best Local Similarity   23.5%;   Score 78.5;   DB 5;   Pred. No. 15;   Length 669;

RESULT 737
ID   ABP28724 standard; protein; 669 AA.
DE   Streptococcus polypeptide SEQ ID NO 6624.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match              6.6%;
     Best Local Similarity   23.5%;   Score 78.5;   DB 5;   Pred. No. 15;   Length 669;

RESULT 738
ID   ADI21047 standard; protein; 703 AA.
DE   Novel human protein #22.
PN   WO200325148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 7;   Pred. No. 16;   Length 703;

RESULT 739
ID   ABM84882 standard; protein; 711 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5131.
PN   WO200423973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 8;   Pred. No. 16;   Length 711;

RESULT 740
ID   ABP52105 standard; protein; 723 AA.
DE   Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
PN   EP1217066-A1.
PD   26-JUN-2002.
PA   (UYGE-) UNIV GENT.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 5;   Pred. No. 16;   Length 723;

RESULT 741
ID   ADQ97094 standard; protein; 723 AA.
DE   Human cancer associated sequence HP1-10-005, SEQ ID 70.
PN   WO2004060304-A2.
PD   22-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 8;   Pred. No. 16;   Length 723;

RESULT 742
ID   AAE02437 standard; protein; 766 AA.
DE   Human ATP binding cassette, ABCB9 transporter protein.
PN   WO200140305-A1.
PD   07-JUN-2001.
PA   (ACTI-) ACTIVE PASS PHARM INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 4;   Pred. No. 18;   Length 766;

RESULT 743
ID   AAE02441 standard; protein; 766 AA.
DE   Human ATP binding cassette, ABCB9 transporter protein mutant K545R.
PN   WO200140305-A1.
PD   07-JUN-2001.
PA   (ACTI-) ACTIVE PASS PHARM INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 4;   Pred. No. 18;   Length 766;

RESULT 744
ID   AAE02442 standard; protein; 766 AA.
DE   Human ATP binding cassette, ABCB9 transporter protein mutant D667N.
PN   WO200140305-A1.
PD   07-JUN-2001.
PA   (ACTI-) ACTIVE PASS PHARM INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 4;   Pred. No. 18;   Length 766;

RESULT 745
ID   AAG67163 standard; protein; 766 AA.
DE   Amino acid sequence of a human 33894 transporter polypeptide.
PN   WO200164875-A2.
PD   07-SEP-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 4;   Pred. No. 18;   Length 766;

RESULT 746
ID   AAG79246 standard; protein; 766 AA.
DE   Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.
PN   WO200173018-A2.
PD   04-OCT-2001.
PA   (MERE ) MERCK PATENT GMBH.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 4;   Pred. No. 18;   Length 766;

RESULT 747
ID   ABB98345 standard; protein; 766 AA.
DE   Human ABC transporter ABCB9 SEQ ID NO 6.
PN   WO200264781-A2.
PD   22-AUG-2002.
PA   (ACTI-) ACTIVE PASS PHARM INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 5;   Pred. No. 18;   Length 766;

RESULT 748
ID   AAE21170 standard; protein; 766 AA.
DE   Human TRICH-14 protein.
PN   WO200212340-A2.
PD   14-FEB-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 5;   Pred. No. 18;   Length 766;

RESULT 749
ID   ADQ97096 standard; protein; 766 AA.
DE   Human cancer associated sequence HP2-10-005, SEQ ID 72.
PN   WO2004060304-A2.
PD   22-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match              6.6%;
     Best Local Similarity   18.0%;   Score 78.5;   DB 8;   Pred. No. 18;   Length 766;

RESULT 750
ID   AAG20805 standard; protein; 377 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
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PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match
     Best Local Similarity   6.5%;   Score 78;   DB 3;   Length 377;
RESULT 751
ID   AAG20804 standard; protein; 442 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (ELIT-) ELITRA PHARM INC.
PD   03-OCT-2002.
     Query Match
     Best Local Similarity   23.8%;   Score 78;   DB 3;   Length 442;
RESULT 752
ID   AAU35545 standard; protein; 471 AA.
DE   Haemophilus influenzae cellular proliferation protein #186.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   25.0%;   Score 78;   DB 3;   Length 471;
RESULT 753
ID   ABU30411 standard; protein; 471 AA.
DE   Protein encoded by Prokaryotic essential gene #15938.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   23.8%;   Score 78;   DB 4;   Length 471;
RESULT 754
ID   AAG20803 standard; protein; 489 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   23.8%;   Score 78;   DB 3;   Length 489;
RESULT 755
ID   ABB49039 standard; protein; 269 AA.
DE   Listeria monocytogenes protein #1743.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST PASTEUR.
     Query Match
     Best Local Similarity   22.0%;   Score 77.5;   DB 5;   Length 269;
RESULT 756
ID   ABG17374 standard; protein; 280 AA.
DE   Novel human diagnostic protein #17365.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   21.9%;   Score 77.5;   DB 4;   Length 280;
RESULT 757
ID   ABU07771 standard; protein; 280 AA.
DE   Polypeptide encoded by novel human contig #22.
PN   WO200302013-A2.
PD   20-MAR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   21.9%;   Score 77.5;   DB 6;   Length 280;
RESULT 758
ID   ABU48889 standard; protein; 327 AA.
DE   Protein encoded by Prokaryotic essential gene #34416.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   24.8%;   Score 77.5;   DB 6;   Length 327;
RESULT 759
ID   AAW13576 standard; protein; 438 AA.
DE   Mouse Batten disease polypeptide CLN3 homologue.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match
     Best Local Similarity   6.5%;   Score 77.5;   DB 2;   Length 438;
RESULT 760
ID   ADS42965 standard; protein; 491 AA.
DE   Bacterial polypeptide #21395.
PN   US200233675-A1.
PD   18-DEC-2003.
PA   (CAOV/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match
     Best Local Similarity   22.6%;   Score 77;   DB 8;   Length 491;
RESULT 761
ID   ADC42919 standard; protein; 892 AA.
DE   Variola smallpox virus A10L.
PN   WO2003017943-A2.
PD   06-MAR-2003.
PA   (MYRI-) MYRIAD GENETICS INC.
     Query Match
     Best Local Similarity   22.7%;   Score 77.5;   DB 7;   Length 892;
RESULT 762
ID   AAR88413 standard; protein; 353 AA.
DE   High-affinity melatonin-1a receptor.
PN   WO9535320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
     Query Match
     Best Local Similarity   22.1%;   Score 77;   DB 2;   Length 353;
RESULT 763
ID   AAW23958 standard; protein; 353 AA.
DE   Mouse melatonin 1a receptor.
PN   WO9803549-A1.
PD   29-JAN-1998.
PA   (GEHO ) GEN HOSPITAL CORP.
     Query Match
     Best Local Similarity   22.1%;   Score 77;   DB 2;   Length 353;
RESULT 764
ID   ABB07571 standard; protein; 353 AA.
DE   Mouse melatonin 1a (Mel1a) receptor.
PN   US6326526-B1.
PD   04-DEC-2001.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA   (GEHO ) GEN HOSPITAL CORP.
     Query Match
     Best Local Similarity   22.1%;   Score 77;   DB 5;   Length 353;
RESULT 765
ID   AD029553 standard; protein; 353 AA.
DE   Mouse GPCR MTNR1A, SEQ ID NO:655.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match
     Best Local Similarity   22.1%;   Score 77;   DB 8;   Length 353;
RESULT 766
ID   ADM25403 standard; protein; 383 AA.
DE   Hyperthermophile Methanopyrus kandleri protein #9.
PN   WO200307675-A2.
PD   18-SEP-2003.
PA   (FIDE-) FIDELITY SYSTEMS INC.
     Query Match
     Best Local Similarity   24.8%;   Score 77;   DB 7;   Length 383;
RESULT 767
ID   ADQ95948 standard; protein; 490 AA.
DE   T cell activation associated protein #63.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match
     Best Local Similarity   19.5%;   Score 77;   DB 8;   Length 490;
RESULT 768
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ID   ADQ96002 standard; protein; 490 AA.
DE   T cell activation associated protein #90.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match             19.5%;  Score 77;  DB 8;  Length 490;
     Best Local Similarity   20.4%;  Pred. No. 14;

RESULT 769
ID   AAG42521 standard; protein; 648 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 648;
     Best Local Similarity   20.4%;  Pred. No. 21;

RESULT 770
ID   ABU16172 standard; protein; 650 AA.
DE   Protein encoded by Prokaryotic essential gene #1699.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             27.5%;  Score 77;  DB 6;  Length 650;
     Best Local Similarity   27.5%;  Pred. No. 21;

RESULT 771
ID   ABM72713 standard; protein; 650 AA.
DE   Staphylococcus aureus protein #1953.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match             27.5%;  Score 77;  DB 6;  Length 650;
     Best Local Similarity   27.5%;  Pred. No. 23;

RESULT 772
ID   AAG42520 standard; protein; 690 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 690;
     Best Local Similarity   20.4%;  Pred. No. 25;

RESULT 773
ID   AAG42519 standard; protein; 728 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 728;
     Best Local Similarity   20.4%;  Pred. No. 29;

RESULT 774
ID   AAG32549 standard; protein; 805 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39287.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 805;
     Best Local Similarity   20.4%;  Pred. No. 31;

RESULT 775
ID   AAG32548 standard; protein; 847 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 847;
     Best Local Similarity   20.4%;  Pred. No. 38;

RESULT 776
ID   AAG32547 standard; protein; 991 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 991;
     Best Local Similarity   20.4%;  Pred. No. 40;

RESULT 777
ID   ABP52133 standard; protein; 1025 AA.
DE   Plasmodium falciparum multidrug resistance protein SEQ ID NO:85.
PN   EP1217066-A1.
PD   26-JUN-2002.
PA   (UYGE-) UNIV GENT.
     Query Match             20.6%;  Score 77;  DB 5;  Length 1025;
     Best Local Similarity   20.6%;  Pred. No. 40;

RESULT 778
ID   AAG42381 standard; protein; 1047 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 1047;
     Best Local Similarity   20.4%;  Pred. No. 41;

RESULT 779
ID   AAG42380 standard; protein; 1191 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 1191;
     Best Local Similarity   20.4%;  Pred. No. 49;

RESULT 780
ID   AAG42379 standard; protein; 1202 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             20.4%;  Score 77;  DB 3;  Length 1202;
     Best Local Similarity   20.4%;  Pred. No. 50;

RESULT 781
ID   AAR29527 standard; protein; 2510 AA.
DE   HCV antigen T7NI-30.
PN   EP518313-A2.
PD   16-DEC-1992.
PA   (MITU ) MITSUBISHI KASEI CORP.
     Query Match             22.5%;  Score 77;  DB 2;  Length 2510;
     Best Local Similarity   22.5%;  Pred. No. 1.4e+02;

RESULT 782
ID   ADX40818 standard; protein; 3010 AA.
DE   HCV polymerase protein #41.
PN   WO200501250-2-A2.
PD   10-FEB-2005.
     Query Match             22.5%;  Score 77;  DB 9;  Length 3010;
     Best Local Similarity   22.5%;  Pred. No. 1.8e+02;

RESULT 783
ID   ADX40816 standard; protein; 3010 AA.
DE   HCV polymerase protein #39.
PN   WO200501250-2-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
     Query Match             22.5%;  Score 77;  DB 9;  Length 3010;
     Best Local Similarity   22.5%;  Pred. No. 1.8e+02;

RESULT 784
ID   ADT56855 standard; protein; 195 AA.
DE   Plant polypeptide, SEQ ID 6932.
PN   US2004216190-A1.
PD   28-OCT-2004.
PA   (KOVA-/) KOVALIC D K.
     Query Match             22.5%;  Score 76.5;  DB 8;  Length 195;
     Best Local Similarity   25.8%;  Pred. No. 4.6;

RESULT 785
ID   ADF74966 standard; protein; 249 AA.
DE   Human 164-1h protein (SeqID 25).
PN   WO2003097696-A1.
PD   27-NOV-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             23.3%;  Score 76.5;  DB 8;  Length 249;
     Best Local Similarity   25.8%;  Pred. No. 6.4;

RESULT 786
ID   ADC01137 standard; protein; 278 AA.
DE   Enterohaemorragic E. coli O157:H7-specific protein SEQ ID NO: 1181.
PN   JP2002355074-A.
PD   10-DEC-2002.
PA   (UYTS-) UNIV TSUKUBA.
     Query Match             23.3%;  Score 76.5;  DB 7;  Length 278;
     Best Local Similarity   28.5%;  Pred. No. 7.5;

RESULT 787
ID   AB065827 standard; protein; 435 AA.
DE   Klebsiella pneumoniae polypeptide seqid 12344.
PN   US6610836-B1.
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PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   6.4%;
     Best Local Similarity   21.8%;
     Score 76.5; Pred. No. 14; DB 7; Length 435;

RESULT 788
ID   ADF74969 standard; protein; 481 AA.
DE   Human 164-1b protein (SeqID 28).
PN   WO2003097686-A1.
PD   27-NOV-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   6.4%;
     Best Local Similarity   23.3%; Score 76.5; Pred. No. 16; DB 8; Length 481;

RESULT 789
ID   AAR90765 standard; protein; 494 AA.
DE   Human K+ channel 2 mature protein.
PN   WO9603415-A1.
PD   08-FEB-1996.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   6.4%;
     Best Local Similarity   21.3%; Score 76.5; Pred. No. 17; DB 2; Length 494;

RESULT 790
ID   AAW42996 standard; protein; 494 AA.
DE   Putative mature potassium channel 2 protein.
PN   US5710019-A.
PD   20-JAN-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   6.4%;
     Best Local Similarity   21.3%; Score 76.5; Pred. No. 17; DB 2; Length 494;

RESULT 791
ID   ABP58356 standard; protein; 494 AA.
DE   Human potassium channel subunit Kv5.1.
PN   WO200296944-A2.
PD   05-DEC-2002.
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
     Query Match   6.4%;
     Best Local Similarity   21.3%; Score 76.5; Pred. No. 17; DB 6; Length 494;

RESULT 792
ID   ADC99155 standard; protein; 494 AA.
DE   Human mature K+ channel 2 protein.
PN   US20030928295-A1.
PD   15-MAY-2003.
PA   (LIYY/) LI Y.
PA   (ADAM/) ADAMS M D.
PA   (WHIT/) WHITE O R.
     Query Match   6.4%;
     Best Local Similarity   21.3%; Score 76.5; Pred. No. 17; DB 7; Length 494;

RESULT 793
ID   AAW20085 standard; protein; 509 AA.
DE   Helicobacter pylori cytoplasmic protein, 10009666.aa.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR) ASTRA AB.
     Query Match   6.4%;
     Best Local Similarity   19.2%; Score 76.5; Pred. No. 17; DB 2; Length 509;

RESULT 794
ID   ADQ07984 standard; protein; 526 AA.
DE   Human hypothetical protein FLJ20371-encoding cDNA.
PN   WO200406123-A2.
PD   22-JUL-2004.
PA   (EXEL-) EXELIXIS INC.
     Query Match   6.4%;
     Best Local Similarity   15.7%; Score 76.5; Pred. No. 18; DB 8; Length 526;

RESULT 795
ID   ADP25065 standard; protein; 526 AA.
DE   PRO polypeptide SEQ ID NO:2243.
PN   WO200401170-A2.
PD   21-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   6.4%;
     Best Local Similarity   15.7%; Score 76.5; Pred. No. 18; DB 8; Length 526;

RESULT 796
ID   ADU06638 standard; protein; 526 AA.
DE   Novel bronchial cancer-associated human protein SeqID864.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.
     Query Match   6.4%;
     Best Local Similarity   15.7%; Score 76.5; Pred. No. 18; DB 8; Length 526;

RESULT 797
ID   ADB63857 standard; protein; 555 AA.
DE   Human protein encoded by clone ASTRO2OO53430.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
PA   (HELI-) HELIX RES INST.
     Query Match   6.4%;
     Best Local Similarity   23.3%; Score 76.5; Pred. No. 20; DB 7; Length 555;

RESULT 798
ID   ABB08159 standard; protein; 570 AA.
DE   Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).
PN   WO200242330-A2.
PD   30-MAY-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   6.4%;
     Best Local Similarity   23.3%; Score 76.5; Pred. No. 20; DB 5; Length 570;

RESULT 799
ID   AAW20918 standard; protein; 593 AA.
DE   H. pylori transporter protein, 14gp12015orf14.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR) ASTRA AB.
     Query Match   6.4%;
     Best Local Similarity   19.2%; Score 76.5; Pred. No. 21; DB 2; Length 593;

RESULT 800
ID   ADN46225 standard; protein; 615 AA.
DE   Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
PN   WO200402736-A1.
PD   18-MAR-2004.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
     Query Match   6.4%;
     Best Local Similarity   22.6%; Score 76.5; Pred. No. 22; DB 8; Length 615;

RESULT 801
ID   ADN21126 standard; protein; 2539 AA.
DE   Bacterial polypeptide #3779.
PN   US20033233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.4%;
     Best Local Similarity   22.1%; Score 76.5; Pred. No. 1.6e+02; DB 8; Length 2539;

RESULT 802
ID   ADH88107 standard; protein; 195 AA.
DE   Enterococcus faecalis polypeptide #2587.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match   6.4%;
     Best Local Similarity   25.9%; Score 76; Pred. No. 5.2; DB 7; Length 195;

RESULT 803
ID   AAG09592 standard; protein; 274 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.4%;
     Best Local Similarity   26.7%; Score 76; Pred. No. 8.4; DB 3; Length 274;

RESULT 804
ID   AAG09591 standard; protein; 287 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 7585.
PN   EP1033405-A2.
PD   06-SEP-2000.

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Query Match       6.4%;  Score 76;  DB 3;  Length 287;
Best Local Similarity    26.7%;  Pred. No. 8,9;

RESULT 805
ID   ADQ96244 standard; protein; 366 AA.
DE   T cell activation associated protein #211.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.

Query Match       6.4%;  Score 76;  DB 8;  Length 366;
Best Local Similarity    22.0%;  Pred. No. 13;

RESULT 806
ID   ADQ96246 standard; protein; 366 AA.
DE   T cell activation associated protein #212.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.

Query Match       6.4%;  Score 76;  DB 8;  Length 366;
Best Local Similarity    22.0%;  Pred. No. 13;

RESULT 807
ID   ABB89424 standard; protein; 456 AA.
DE   Human polypeptide SEQ ID NO 1800.
PN   WO20019030304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.

Query Match       6.4%;  Score 76;  DB 5;  Length 456;
Best Local Similarity    22.0%;  Pred. No. 17;

RESULT 808
ID   AAB53400 standard; protein; 557 AA.
DE   Human colon cancer antigen protein sequence SEQ ID NO:940.
PN   WO200055351-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.

Query Match       6.4%;  Score 76;  DB 3;  Length 557;
Best Local Similarity    22.0%;  Pred. No. 22;

RESULT 809
ID   AAY44945 standard; protein; 593 AA.
DE   Wheat sulphate permease-2.
PN   WO200004154-A2.
PD   27-JAN-2000.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.

Query Match       6.4%;  Score 76;  DB 3;  Length 593;
Best Local Similarity    21.4%;  Pred. No. 24;

RESULT 810
ID   ADN22849 standard; protein; 1402 AA.
DE   Bacterial polypeptide #5502.
PN   US20023367S-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

Query Match       6.4%;  Score 76;  DB 8;  Length 1402;
Best Local Similarity    21.4%;  Pred. No. 81;

RESULT 811
ID   ADN23383 standard; protein; 1917 AA.
DE   Bacterial polypeptide #6036.
PN   US20023367S-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

Query Match       6.4%;  Score 76;  DB 8;  Length 1917;
Best Local Similarity    20.2%;  Pred. No. 1.2e+02;

RESULT 812
ID   ADX40794 standard; protein; 3010 AA.
DE   HCV polymerase protein #17.
PN   WO200512502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMUNE INC.

Query Match       6.4%;  Score 76;  DB 9;  Length 3010;


Best Local Similarity    25.4%;  Pred. No. 2.3e+02;

RESULT 813
ID   ADX40791 standard; protein; 3010 AA.
DE   HCV polymerase protein #14.
PN   WO200512502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMUNE INC.

Query Match       6.4%;  Score 76;  DB 9;  Length 3010;
Best Local Similarity    25.4%;  Pred. No. 2.3e+02;

RESULT 814
ID   ADX40792 standard; protein; 3010 AA.
DE   HCV polymerase protein #15.
PN   WO200512502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMUNE INC.

Query Match       6.4%;  Score 76;  DB 9;  Length 3010;
Best Local Similarity    26.9%;  Pred. No. 2.3e+02;

RESULT 815
ID   ABB63150 standard; protein; 228 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 16242.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.

Query Match       6.3%;  Score 75.5;  DB 4;  Length 228;
Best Local Similarity    21.8%;  Pred. No. 7,4;

RESULT 816
ID   ADK46633 standard; protein; 263 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 3148.
PN   US6699703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.

Query Match       6.3%;  Score 75.5;  DB 8;  Length 263;
Best Local Similarity    18.0%;  Pred. No. 9,1;

RESULT 817
ID   ADM92206 standard; protein; 263 AA.
DE   S pneumoniae antigenic protein sequence SeqID403.
PN   WO200402060609-A2.
PD   11-MAR-2004.
PA   (TUFT ) UNIV TUFTS.

Query Match       6.3%;  Score 75.5;  DB 3;  Length 263;
Best Local Similarity    18.0%;  Pred. No. 9,1;

RESULT 818
ID   AAY81619 standard; protein; 264 AA.
DE   Streptococcus pneumoniae type 4 protein sequence #119.
PN   WO200006737-A2.
PD   10-FEB-2000.
PA   (MICR-) MICROBIAL TECHNICS LTD.

Query Match       6.3%;  Score 75.5;  DB 3;  Length 264;
Best Local Similarity    18.0%;  Pred. No. 9,1;

RESULT 819
ID   ADR96242 standard; protein; 264 AA.
DE   Novel S. pneumoniae protein sequence, SEQ ID 4877.
PN   US6800744-B1.
PD   05-OCT-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.

Query Match       6.3%;  Score 75.5;  DB 8;  Length 264;
Best Local Similarity    18.0%;  Pred. No. 9,1;

RESULT 820
ID   AEA60112 standard; protein; 264 AA.
DE   Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4877.
PN   US20051364404-A1.
PD   23-JUN-2005.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.

Query Match       6.3%;  Score 75.5;  DB 9;  Length 264;
Best Local Similarity    18.0%;  Pred. No. 9,1;

RESULT 821
ID   ABU02182 standard; protein; 276 AA.
DE   S. pneumoniae type 4 strain protein from coding region #1759.
PN   WO200277021-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
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RESULT 822
Query Match   6.3%;   Score 75.5; DB 6; Length 276;
Best Local Similarity   18.0%; Pred. No. 9.7;
ID ABG93285 standard; protein; 342 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 528.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
PA

RESULT 823
Query Match   6.3%;   Score 75.5; DB 5; Length 342;
Best Local Similarity   21.9%; Pred. No. 13;
ID AAB15936 standard; protein; 352 AA.
DE E. coli proliferation associated protein sequence SEQ ID NO:293.
PN WO200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.

RESULT 824
Query Match   6.3%;   Score 75.5; DB 3; Length 352;
Best Local Similarity   31.7%; Pred. No. 14;
ID ADH51470 standard; protein; 363 AA.
DE Rat MT1 receptor amino acid sequence #SEQ ID 2.
PN FR2835847-A1.
PD 15-AUG-2003.
PA (SERV-) LES LAB SERVIER SA.

RESULT 825
Query Match   6.3%;   Score 75.5; DB 7; Length 363;
Best Local Similarity   23.5%; Pred. No. 14;
ID AAU03851 standard; protein; 397 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.

RESULT 826
Query Match   6.3%;   Score 75.5; DB 9; Length 397;
Best Local Similarity   19.1%; Pred. No. 16;
ID ADU92092 standard; protein; 415 AA.
DE Escherichia coli TnaB protein.
PN EP1484410-A1.
PD 08-DEC-2004.
PA (AJIN) AJINOMOTO KK.

RESULT 827
Query Match   6.3%;   Score 75.5; DB 9; Length 415;
Best Local Similarity   20.5%; Pred. No. 17;
ID AEB41698 standard; protein; 430 AA.
DE L. pneumophila protein SEQ ID NO 6030.
PN WO200549642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.

RESULT 828
Query Match   6.3%;   Score 75.5; DB 4; Length 430;
Best Local Similarity   25.5%; Pred. No. 18;
ID AAU03852 standard; protein; 433 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #24.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.

RESULT 829
Query Match   6.3%;   Score 75.5; DB 4; Length 433;
Best Local Similarity   19.1%; Pred. No. 18;
ID AEB38437 standard; protein; 436 AA.
DE L. pneumophila protein SEQ ID NO 2769.
PN WO200549642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.

RESULT 830
Query Match   6.3%;   Score 75.5; DB 9; Length 436;
Best Local Similarity   25.5%;

ID ADS24239 standard; protein; 463 AA.
DE Bacterial polypeptide #13272.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

RESULT 831
Query Match   6.3%;   Score 75.5; DB 8; Length 463;
Best Local Similarity   21.4%; Pred. No. 20;
ID ADO29507 standard; protein; 471 AA.
DE Mouse GPCR HTR2A, SEQ ID NO:609.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.

RESULT 832
Query Match   6.3%;   Score 75.5; DB 4; Length 471;
Best Local Similarity   21.0%; Pred. No. 20;
ID AAU03820 standard; protein; 499 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #19.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.

RESULT 833
Query Match   6.3%;   Score 75.5; DB 8; Length 499;
Best Local Similarity   19.1%; Pred. No. 18;
ID ADM72132 standard; protein; 392 AA.
DE Human NTRAN polypeptide (clone ID 752455CD1).
PN WO2004022705-A2.
PD 18-MAR-2004.
PA (INCY-) INCYTE CORP.

RESULT 834
Query Match   6.3%;   Score 75.5; DB 7; Length 392;
Best Local Similarity   21.0%; Pred. No. 19;
ID ABM90212 standard; protein; 404 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO 3554.
PN WO200300540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

RESULT 835
Query Match   6.3%;   Score 75.5; DB 8; Length 404;
Best Local Similarity   15.6%; Pred. No. 18;
ID AEB39222 standard; protein; 418 AA.
DE L. pneumophila protein SEQ ID NO 3554.
PN WO200549642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.

RESULT 836
Query Match   6.3%;   Score 75; DB 9; Length 418;
Best Local Similarity   20.7%; Pred. No. 21;
ID AEB35772 standard; protein; 437 AA.
DE L. pneumophila protein SEQ ID NO 104.
PN WO200549642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.

RESULT 837
Query Match   6.3%;   Score 75; DB 4; Length 437;
Best Local Similarity   20.7%; Pred. No. 21;
ID AAU45917 standard; protein; 445 AA.
DE Propionibacterium acnes immunogenic protein #6813.
PN WO200181581-A1.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match   6.3%;   Score 75; DB 4; Length 445;
Best Local Similarity   24.8%;

RESULT 838
ID   ABM42436 standard; protein; 445 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
PN   WO200303515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
     Query Match   6.3%; Score 75; DB 6; Length 445;
     Best Local Similarity   24.8%; Pred. No. 22;

RESULT 839
ID   ABM87563 standard; protein; 452 AA.
DE   Rice abiotic stress responsive polypeptide SEQ ID NO:5809.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
     Query Match   6.3%; Score 75; DB 7; Length 452;
     Best Local Similarity   15.6%; Pred. No. 22;

RESULT 840
ID   ADA34178 standard; protein; 467 AA.
DE   Acinetobacter baumannii protein #1139.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   6.3%; Score 75; DB 6; Length 467;
     Best Local Similarity   23.1%; Pred. No. 23;

RESULT 841
ID   ADR14597 standard; protein; 473 AA.
DE   Human NF-kappaB pathway-associated protein SeqID598.
PN   WO2004065577-A2.
PD   05-AUG-2004.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
     Query Match   6.3%; Score 75; DB 8; Length 473;
     Best Local Similarity   21.0%; Pred. No. 23;

RESULT 842
ID   ADP99138 standard; protein; 480 AA.
DE   Human transporter and ion channel (TRICH) protein - SEQ ID 3.
PN   WO2004048599-A2.
PD   10-JUN-2004.
PA   (INCY-) INCYTE CORP.
     Query Match   6.3%; Score 75; DB 8; Length 480;
     Best Local Similarity   21.0%; Pred. No. 24;

RESULT 843
ID   ADH86490 standard; protein; 549 AA.
DE   Enterococcus faecalis polypeptide #970.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match   6.3%; Score 75; DB 7; Length 549;
     Best Local Similarity   18.7%; Pred. No. 29;

RESULT 844
ID   ADX80121 standard; protein; 635 AA.
DE   Plant full length insert polypeptide seqid 49487.
PN   US200403488-A1.
PD   19-FEB-2004.
PA   (LIU/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   6.3%; Score 75; DB 8; Length 635;
     Best Local Similarity   25.3%; Pred. No. 35;

RESULT 845
ID   AAR54066 standard; protein; 1051 AA.
DE   Non-A, non-B hepatitis virus gene #4 product.
PN   JP06141870-A.
PD   24-MAY-1994.
PA   (TOKR/) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA   (SANW) SANWA KAGAKU KENKYUSHO CO.
PA   (TOFU) TONEN CORP.
     Query Match   6.3%; Score 75; DB 2; Length 1051;
     Best Local Similarity   23.4%; Pred. No. 71;

RESULT 846
ID   AAR98361 standard; protein; 1051 AA.
DE   5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
PN   JP07133291-A.
PD   23-MAY-1995.
PA   (TOFU) TONEN CORP.
     Query Match   6.3%; Score 75; DB 2; Length 1051;
     Best Local Similarity   23.4%; Pred. No. 71;

RESULT 847
ID   ADB64712 standard; protein; 1131 AA.
DE   Human protein encoded by clone NT2NE20077270.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match   6.3%; Score 75; DB 7; Length 1131;
     Best Local Similarity   23.9%; Pred. No. 79;

RESULT 848
ID   ABB64494 standard; protein; 2248 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 20274.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.3%; Score 75; DB 4; Length 2248;
     Best Local Similarity   22.9%; Pred. No. 2e+02;

RESULT 849
ID   ADG20763 standard; protein; 2248 AA.
DE   Drosophila melanogaster rutabaga protein SEQ ID NO:2.
PN   WO2003103704-A2.
PD   18-DEC-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
     Query Match   6.3%; Score 75; DB 8; Length 2248;
     Best Local Similarity   22.9%; Pred. No. 2e+02;

RESULT 850
ID   ADQ89656 standard; protein; 2248 AA.
DE   Antagonist of cell cycle progression polypeptide #43.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.
     Query Match   6.3%; Score 75; DB 8; Length 2248;
     Best Local Similarity   22.9%; Pred. No. 2e+02;

RESULT 851
ID   ADX40796 standard; protein; 3010 AA.
DE   HCV polymerase protein #19.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
     Query Match   6.3%; Score 75; DB 9; Length 3010;
     Best Local Similarity   25.4%; Pred. No. 3.1e+02;

RESULT 852
ID   AAB66797 standard; protein; 200 AA.
DE   Porcine reproductive and respiratory syndrome virus ORF #5 protein.
PN   WO2002102858-A1.
PD   11-JAN-2001.
PA   (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA   (MATE-) INST MATERIALS RES & ENG.
     Query Match   6.2%; Score 74.5; DB 4; Length 200;
     Best Local Similarity   23.8%; Pred. No. 8.1;

RESULT 853
ID   ADF74954 standard; protein; 256 AA.
DE   Rat 164-1h protein (SeqID 13).
PN   WO2003097686-A1.
PD   27-NOV-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   6.2%; Score 74.5; DB 8; Length 256;
     Best Local Similarity   23.3%; Pred. No. 11;

RESULT 854
ID   AAR53748 standard; protein; 355 AA.
DE   Seven transmembrane receptor (V28).
PN   WO9412635-A2.
PD   09-JUN-1994.
PA   (ICOS-) ICOS CORP.
     Query Match   6.2%; Score 74.5; DB 2; Length 355;
     Best Local Similarity   25.8%; Pred. No. 18;

RESULT 855
ID AAW48722 standard; protein; 355 AA.
DE Human V28 seven transmembrane receptor.
PN US575804-A.
PD 02-JUN-1998.
PA (ICOS-) ICOS CORP.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 2; Length 355;

RESULT 856
ID AAY90677 standard; protein; 355 AA.
DE Human mutant G protein-coupled receptor V28 (I230K).
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 3; Length 355;

RESULT 857
ID AAY90642 standard; protein; 355 AA.
DE Human G protein-coupled receptor V28.
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 3; Length 355;

RESULT 858
ID AAB21693 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #2.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 3; Length 355;

RESULT 859
ID AAB21692 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #1.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 3; Length 355;

RESULT 860
ID AAG80126 standard; protein; 355 AA.
DE Human CX3CR1 protein.
PN WO200172830-A2.
PD 04-OCT-2001.
PA (IPFP-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 4; Length 355;

RESULT 861
ID AAB82786 standard; protein; 355 AA.
DE Human CX3C chemokine receptor 1.
PN WO200160406-A1.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PHARM INC.
PA (NOUN) UNIV NORTHWESTERN.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 4; Length 355;

RESULT 862
ID AAU91235 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #2.
PN US6348574-B1.
PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 5; Length 355;

RESULT 863
ID AAU91234 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #1.
PN US6348574-B1.
PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 5; Length 355;

RESULT 864
ID AAU84327 standard; protein; 355 AA.
DE Protein CX3CR1 differentially expressed in breast cancer tissue.
PN WO200210436-A2.
PD 07-FEB-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA (BAAK/) BAAK J.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 5; Length 355;

RESULT 865
ID ABR58524 standard; protein; 355 AA.
DE Human chemokine (C-X3-C) receptor 1 protein.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 6; Length 355;

RESULT 866
ID AAO29513 standard; protein; 355 AA.
DE Human fractalkine receptor (313) protein.
PN WO2003039475-A2.
PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 6; Length 355;

RESULT 867
ID ABP97732 standard; protein; 355 AA.
DE Amino acid sequence of human chemokine receptor CX3CR1.
PN WO2003014153-A2.
PD 20-FEB-2003.
PA (TOPI-) TOPIGEN PHARM INC.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 6; Length 355;

RESULT 868
ID ABP81882 standard; protein; 355 AA.
DE Human chemokine fractalkine receptor 1 protein SEQ ID NO:249.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 6; Length 355;

RESULT 869
ID ADC22751 standard; protein; 355 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #74.
PN US6553339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 7; Length 355;

RESULT 870
ID ADC22649 standard; protein; 355 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #34.
PN US6553339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 7; Length 355;

RESULT 871
ID ADH14224 standard; protein; 355 AA.
DE Mutated human serotonin V28.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match
Best Local Similarity   25.8%;
Score 74.5; DB 7; Length 355;

RESULT 872
ID ADH14122 standard; protein; 355 AA.
DE Human serotonin V28.
PN US2003105292-A1.
PD 05-JUN-2003.

PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
PA   Query Match   25.8%;   Score 74.5;   DB 7;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 873
ID   ADH10680 standard; protein; 355 AA.
DE   Human CX3CR1 polypeptide.
PN   WO200310484-A1.
PD   18-DEC-2003.
PA   (META-) METABOLEX INC.
      Query Match   25.8%;   Score 74.5;   DB 8;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 874
ID   ADQ29269 standard; protein; 355 AA.
DE   Human GPCR CX3CR1, SEQ ID NO:370.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
      Query Match   25.8%;   Score 74.5;   DB 8;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 875
ID   ADQ18141 standard; protein; 355 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 958.
PN   WO200404938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
      Query Match   25.8%;   Score 74.5;   DB 8;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 876
ID   ADP56020 standard; protein; 355 AA.
DE   Human PRO protein sequence SEQ ID NO:1996.
PN   WO200403956-A2.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
      Query Match   25.8%;   Score 74.5;   DB 8;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 877
ID   ADP54585 standard; protein; 355 AA.
DE   Human PRO protein sequence SEQ ID NO:561.
PN   WO200403956-A2.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
      Query Match   25.8%;   Score 74.5;   DB 8;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 878
ID   ADP5421 standard; protein; 355 AA.
DE   PRO polypeptide SEQ ID NO:1109.
PN   WO200405852-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
      Query Match   25.8%;   Score 74.5;   DB 8;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 879
ID   ADQ39421 standard; protein; 355 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1084.
PN   WO200405852-A2.
PD   21-MAY-2004.
PA   (GETH) GENENTECH INC.
      Query Match   25.8%;   Score 74.5;   DB 9;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 880
ID   ADY15644 standard; protein; 355 AA.
DE   PRO polypeptide SEQ ID NO 1450.
PN   WO200501962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
      Query Match   25.8%;   Score 74.5;   DB 4;   Length 355;
      Best Local Similarity   25.8%;   Pred. No. 18;
RESULT 881
ID   ADQ39422 standard; protein; 362 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1085.
PN   WO200405852-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
      Query Match   25.8%;   Score 74.5;   DB 8;   Length 362;
      Best Local Similarity   25.8%;   Pred. No. 19;
RESULT 882
ID   AAW77109 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322K mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.
      Query Match   21.0%;   Score 74.5;   DB 2;   Length 471;
      Best Local Similarity   21.0%;   Pred. No. 27;
RESULT 883
ID   AAW77111 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322E mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.
      Query Match   21.0%;   Score 74.5;   DB 2;   Length 471;
      Best Local Similarity   21.0%;   Pred. No. 27;
RESULT 884
ID   AAW77110 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322R mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.
      Query Match   21.0%;   Score 74.5;   DB 2;   Length 471;
      Best Local Similarity   21.0%;   Pred. No. 27;
RESULT 885
ID   AAW77104 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.
      Query Match   21.0%;   Score 74.5;   DB 2;   Length 471;
      Best Local Similarity   21.0%;   Pred. No. 27;
RESULT 886
ID   ABB07980 standard; protein; 471 AA.
DE   Rat 5-HT2 receptor sequence.
PN   US6383762-B1.
PD   07-MAY-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.
      Query Match   21.0%;   Score 74.5;   DB 5;   Length 471;
      Best Local Similarity   21.0%;   Pred. No. 27;
RESULT 887
ID   ADF74971 standard; protein; 481 AA.
DE   Rat 164-1b protein (SeqID 30).
PN   WO200309786-A1.
PD   27-NOV-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   21.0%;   Score 74.5;   DB 8;   Length 481;
      Best Local Similarity   21.0%;   Pred. No. 27;
RESULT 888
ID   AAM93692 standard; protein; 562 AA.
DE   Human polypeptide, SEQ ID NO: 3602.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
      Query Match   23.3%;   Score 74.5;   DB 8;   Length 562;
      Best Local Similarity   23.3%;   Pred. No. 27;
RESULT 889
ID   ADL31569 standard; protein; 562 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3602.
PN   EP1396543-A2.
PD   10-MAR-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.2%; Pred. No. 34;
Best Local Similarity 23.1%; Score 74.5; DB 8; Length 562;
PN WO20040058805-A2.
DE T cell activation associated protein #158.
ID ADQ96138 standard; protein; 562 AA.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.

RESULT 890
Query Match 6.2%; Pred. No. 36;
Best Local Similarity 18.2%; Score 74.5; DB 8; Length 587;
PN WO20040067709-A2.
DE Aspergillus fumigatus essential gene protein #210.
ID ADR86160 standard; protein; 587 AA.
PD 12-AUG-2004.
PA (ELIT-) ELITRA CANADA LTD.

RESULT 891
Query Match 6.2%; Pred. No. 37;
Best Local Similarity 27.2%; Score 74.5; DB 4; Length 597;
PN WO20020171042-A2.
DE Drosophila melanogaster polypeptide SEQ ID NO 15636.
ID ABB62948 standard; protein; 597 AA.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.

RESULT 892
Query Match 6.2%; Pred. No. 43;
Best Local Similarity 20.4%; Score 74.5; DB 8; Length 661;
PN US20040034888-A1.
DE Plant full length insert polypeptide seqid 37283.
ID ADX66440 standard; protein; 661 AA.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.

RESULT 893
Query Match 6.2%; Pred. No. 70;
Best Local Similarity 21.1%; Score 74.5; DB 6; Length 940;
PN US6562958-B1.
DE Acinetobacter baumannii protein #4039.
ID ADA36878 standard; protein; 940 AA.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

RESULT 894
Query Match 6.2%; Pred. No. 1.7e+02;
Best Local Similarity 21.1%; Score 74.5; DB 5; Length 1808;
PN WO20020210210-A2.
DE Herbicidally active polypeptide SEQ ID NO 1942.
ID ABB92731 standard; protein; 1808 AA.
PD 07-FEB-2002.
PA (FARB) BAYER AG.

RESULT 895
Query Match 6.2%;
Best Local Similarity 17.3%; Score 74.5; DB 5; Length 3010;
PN WO20020208447-A2.
DE HCV-S1 full-length polyprotein.
ID AAE20477 standard; protein; 3010 AA.
PD 31-JAN-2002.
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.

RESULT 896
Query Match 6.2%; Pred. No. 3.5e+02;
Best Local Similarity 23.8%; Score 74; DB 7; Length 154;
PN US6605709-B1.
DE Bacterial polypeptide #3407.
ID ADF07294 standard; protein; 154 AA.
PD 12-AUG-2003.
PA (EHRL/) EHRLICH G.

RESULT 897
Query Match
PA (GENO-) GENOME THERAPEUTICS CORP.

Best Local Similarity 26.4%; Pred. No. 6.5;

RESULT 898
Query Match 6.2%; Pred. No. 11;
Best Local Similarity 18.5%; Score 74; DB 6; Length 231;
PN WO2002086122-A2.
DE Human adipocyte bait protein, melatonin receptor_V4.
ID ABU70365 standard; protein; 231 AA.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.

RESULT 899
Query Match 6.2%; Pred. No. 11;
Best Local Similarity 18.5%; Score 74; DB 6; Length 231;
PN WO2002086122-A2.
DE Human adipocyte bait protein, melatonin receptor_V5.
ID ABU70366 standard; protein; 231 AA.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.

RESULT 900
Query Match 6.2%; Pred. No. 17;
Best Local Similarity 24.3%; Score 74; DB 5; Length 312;
PN FR2807446-A1.
DE Lactococcus lactis protein yilG.
ID ABS54180 standard; protein; 312 AA.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

RESULT 901
Query Match 6.2%; Pred. No. 17;
Best Local Similarity 38.3%; Score 74; DB 8; Length 312;
PN US20032233675-A1.
DE Bacterial polypeptide #22913.
ID ADS44483 standard; protein; 312 AA.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

RESULT 902
Query Match 6.2%; Pred. No. 18;
Best Local Similarity 24.3%; Score 74; DB 6; Length 324;
PN WO2002077021-A2.
DE S. pneumoniae type 4 strain protein from coding region #2450.
ID ABU02869 standard; protein; 324 AA.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.

RESULT 903
Query Match 6.2%; Pred. No. 19;
Best Local Similarity 24.3%; Score 74; DB 8; Length 332;
PN US6800744-B1.
DE Novel S. pneumoniae protein sequence, SEQ ID 2662.
ID ADR94027 standard; protein; 332 AA.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.

RESULT 904
Query Match 6.2%; Pred. No. 19;
Best Local Similarity 24.3%; Score 74; DB 9; Length 332;
PN US2005136404-A1.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:2662.
ID AEA57897 standard; protein; 332 AA.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.

RESULT 905
Query Match 6.2%; Pred. No. 20;
Best Local Similarity 21.2%; Score 74; DB 6; Length 342;
PN WO20030232013-A2.
DE Novel human polypeptide #35.
ID ABO00448 standard; protein; 342 AA.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.

RESULT 906
Query Match
Best Local Similarity
ID AAR88412 standard; protein; 350 AA.

[RESULT — bibliographic continued from previous page]
DE High-affinity melatonin-1a receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.2%;
Best Local Similarity 18.5%; Score 74; DB 2; Length 350; Pred. No. 20;

RESULT 907
ID AAW15786 standard; protein; 350 AA.
DE Melatonin receptor protein.
PN JP09084581-A.
PD 31-MAR-1997.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.2%;
Best Local Similarity 18.5%; Score 74; DB 2; Length 350; Pred. No. 20;

RESULT 908
ID AAW94761 standard; protein; 350 AA.
DE Human melatonin receptor protein.
PN EP892046-A2.
PD 20-JAN-1999.
PA (JCRP-) JCR PHARM CO LTD.
Query Match 6.2%;
Best Local Similarity 18.5%; Score 74; DB 6; Length 350; Pred. No. 20;

RESULT 909
ID ABP81840 standard; protein; 350 AA.
DE Human melatonin receptor protein type 1a protein SEQ ID NO:164.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.2%;
Best Local Similarity 18.5%; Score 74; DB 8; Length 350; Pred. No. 20;

RESULT 910
ID ADO29552 standard; protein; 350 AA.
DE Human GPCR MTNR1A, SEQ ID NO:654.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.2%;
Best Local Similarity 18.5%; Score 74; DB 6; Length 350; Pred. No. 20;

RESULT 911
ID AAW19220 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor type Ia.
PN WO9721730-A1.
PD 19-JUN-1997.
PA (MERI) MERCK & CO INC.
Query Match 6.2%;
Best Local Similarity 19.4%; Score 74; DB 2; Length 364; Pred. No. 21;

RESULT 912
ID ABM73179 standard; protein; 366 AA.
DE Staphylococcus aureus protein #2419.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%;
Best Local Similarity 21.8%; Score 74; DB 6; Length 366; Pred. No. 22;

RESULT 913
ID ABB55224 standard; protein; 442 AA.
DE Lactococcus lactis protein yteb.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRA) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.2%;
Best Local Similarity 20.4%; Score 74; DB 5; Length 442; Pred. No. 28;

RESULT 914
ID ADN23927 standard; protein; 485 AA.
DE Bacterial polypeptide #6580.
PN US20032336575-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%;
Best Local Similarity 26.2%; Score 74; DB 8; Length 485; Pred. No. 32;

RESULT 915
ID AAY80509 standard; protein; 492 AA.
DE F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
PN WO200008170-A1.
PD 17-FEB-2000.
PA (SAQC) MERCIAN CORP.
Query Match 6.2%;
Best Local Similarity 22.5%; Score 74; DB 3; Length 492; Pred. No. 32;

RESULT 916
ID AAG64105 standard; protein; 493 AA.
DE Flavobacterium lutescens L-lysine-6-aminotransferase.
PN JP06141870-A.
PD 24-MAY-1994.
PA (SAOC) MERCIAN CORP.
Query Match 6.2%;
Best Local Similarity 22.5%; Score 74; DB 4; Length 493; Pred. No. 33;

RESULT 917
ID AAR54067 standard; protein; 1031 AA.
DE Non-A, non-B hepatitis virus gene #6 product.
PN JP07133291-A.
PD 23-MAY-1995.
PA (TOFU) TONEN CORP.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
Query Match 6.2%;
Best Local Similarity 26.2%; Score 74; DB 2; Length 1031; Pred. No. 91;

RESULT 918
ID AAR98362 standard; protein; 1031 AA.
DE 5'/UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).
PN EP1033405-A2.
PD 06-SEP-2000.
PA (TOFU) TONEN CORP.
Query Match 6.2%;
Best Local Similarity 20.3%; Score 73.5; DB 3; Length 120; Pred. No. 5.3;

RESULT 919
ID AAG59839 standard; protein; 120 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (TOFU) TONEN CORP.
Query Match 6.2%;
Best Local Similarity 26.2%; Score 74; DB 2; Length 1031; Pred. No. 91;

RESULT 920
ID AAU25578 standard; protein; 192 AA.
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #25.
PN WO200162797-A2.
PD 30-AUG-2001.
PA (PHA) PHARMACIA & UPJOHN CO.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.2%;
Best Local Similarity 26.3%; Score 73.5; DB 4; Length 192; Pred. No. 10;

RESULT 921
ID ADU08915 standard; protein; 226 AA.
DE Coronavirus membrane protein seqid 38.
PN WO2004096842-A2.
PD 11-NOV-2004.
PA (BCCA-) BC CANCER AGENCY.
Query Match 6.2%;
Best Local Similarity 22.2%; Score 73.5; DB 8; Length 226; Pred. No. 13;

RESULT 922
ID ABU44044 standard; protein; 268 AA.
DE Protein encoded by Prokaryotic essential gene #29571.
PN WO200027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%;
Best Local Similarity 19.6%; Score 73.5; DB 6; Length 268; Pred. No. 16;

RESULT 923
ID AAG32488 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (TOFU) TONEN CORP.
Query Match 6.2%;
Best Local Similarity 28.1%; Score 73.5; DB 3; Length 282; Pred. No. 17;

RESULT 924
ID   ADF05902 standard; protein; 312 AA.
DE   Bacterial polypeptide #2095.
PN   US6605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   6.2%; Score 73.5; DB 7; Length 312;
     Best Local Similarity   17.4%; Pred. No. 20;

RESULT 925
ID   AAG51386 standard; protein; 377 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 377;
     Best Local Similarity   28.1%; Pred. No. 26;

RESULT 926
ID   AAG32487 standard; protein; 377 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 377;
     Best Local Similarity   28.1%; Pred. No. 26;

RESULT 927
ID   ABM92289 standard; protein; 400 AA.
DE   M. xanthus protein sequence, seq id 11488.
PN   US6833447-B1.
PD   21-DEC-2004.
PA   (MONS) MONSANTO TECHNOLOGY LLC.
     Query Match   6.2%; Score 73.5; DB 9; Length 400;
     Best Local Similarity   23.3%; Pred. No. 28;

RESULT 928
ID   ADQ75734 standard; protein; 404 AA.
DE   Codon optimised hCMV IE1 encoded exons 2 and 4.
PN   WO2004058166-A2.
PD   15-JUL-2004.
PA   (VICA-) VICAL INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 404;
     Best Local Similarity   19.3%; Pred. No. 28;

RESULT 929
ID   AAG51385 standard; protein; 442 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 442;
     Best Local Similarity   28.1%; Pred. No. 32;

RESULT 930
ID   AAG32486 standard; protein; 442 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 442;
     Best Local Similarity   28.1%; Pred. No. 32;

RESULT 931
ID   AAG51384 standard; protein; 489 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 489;
     Best Local Similarity   28.1%; Pred. No. 37;

RESULT 932
ID   AAB86544 standard; protein; 491 AA.
DE   Human Cytomegalovirus strain AD169 IE1 protein.
PN   WO200163286-A2.
PD   30-AUG-2001.
PA   (KERN/) KERN F.
     Query Match   6.2%; Score 73.5; DB 4; Length 491;
     Best Local Similarity   19.3%; Pred. No. 37;

RESULT 933
ID   ADP12517 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #127.
PN   WO2004042346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.

RESULT 934
ID   ADP12518 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #128.
PN   WO2004042346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 37;

RESULT 935
ID   ADP12513 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #123.
PN   WO2004042346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 37;

RESULT 936
ID   ADP12514 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #124.
PN   WO2004042346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 37;

RESULT 937
ID   ADQ75725 standard; protein; 491 AA.
DE   Wild type hCMV IE1.
PN   WO2004058166-A2.
PD   15-JUL-2004.
PA   (VICA-) VICAL INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 37;

RESULT 938
ID   ABP73574 standard; protein; 574 AA.
DE   Candida albicans essential protein SEQ ID NO 7411.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.2%; Score 73.5; DB 5; Length 574;
     Best Local Similarity   20.8%; Pred. No. 46;

RESULT 939
ID   ADS28278 standard; protein; 637 AA.
DE   Bacterial polypeptide #17311.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.2%; Score 73.5; DB 4; Length 637;
     Best Local Similarity   28.3%; Pred. No. 53;

RESULT 940
ID   ABG29128 standard; protein; 682 AA.
DE   Novel human diagnostic protein #29119.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.2%; Score 73.5; DB 4; Length 682;
     Best Local Similarity   20.0%; Pred. No. 58;

RESULT 941
ID   ABB61737 standard; protein; 1287 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 12003.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   6.2%; Score 73.5; DB 4; Length 1287;
     Best Local Similarity   18.2%; Pred. No. 1.4e+02;

RESULT 942
ID   ADS96670 standard; protein; 1287 AA.
DE   Drosophila melanogaster protein, SEQ ID 291.

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PN   WO200403999-A2.
PD   13-MAY-2004.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
     Query Match             6.2%;
     Best Local Similarity   18.2%;   Score 73.5;   Pred. No. 1.4e+02;   DB 8;   Length 1287;

RESULT 943
ID   AAR33214 standard; protein; 3033 AA.
DE   NANBH virus strain HC-J8 protein.
PN   EP532167-A2.
PD   17-MAR-1993.
PA   (IMMO ) IMMUNO JAPAN INC.
     Query Match             6.2%;
     Best Local Similarity   6.2%;    Score 73.5;   Pred. No. 4.6e+02;   DB 2;   Length 3033;

RESULT 944
ID   ABY03151 standard; protein; 7176 AA.
DE   Murine hepatitis virus pol1ab protein, SEQ:9897.
PN   WO2004092360-A2.
PD   28-OCT-2004.
PA   (CHIR ) CHIRON CORP.
     Query Match             6.2%;
     Best Local Similarity   27.4%;   Score 73.5;   Pred. No. 1.5e+03;   DB 8;   Length 7176;

RESULT 945
ID   AAW20571 standard; protein; 114 AA.
DE   H pylori secreted or periplasmic protein 80257.aa.
PN   WO9640899-A1.
PD   19-DEC-1996.
PA   (ASTR ) ASTRA AB.
     Query Match             6.2%;
     Best Local Similarity   26.4%;   Score 73.5;   Pred. No. 5.6e+03;   DB 8;   Length 114;

RESULT 946
ID   AAU69567 standard; protein; 189 AA.
DE   Human G protein-coupled receptor from cDNA Seq-2643.
PN   WO200017330-A2.
PD   18-OCT-2001.
PA   (PHA ) PHARMACIA & UPJOHN CO.
     Query Match             6.1%;
     Best Local Similarity   21.6%;   Score 73;   Pred. No. 11;   DB 2;   Length 189;

RESULT 947
ID   ADC97146 standard; protein; 199 AA.
DE   E. faecium protein sequence SEQ ID 6773.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match             6.1%;
     Best Local Similarity   20.3%;   Score 73;   Pred. No. 12;   DB 5;   Length 199;

RESULT 948
ID   ABP29367 standard; protein; 249 AA.
DE   Streptococcus polypeptide SEQ ID NO 7910.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match             6.1%;
     Best Local Similarity   22.6%;   Score 73;   Pred. No. 17;   DB 7;   Length 249;

RESULT 949
ID   AAU87836 standard; protein; 272 AA.
DE   T. aureum 7091 elongase TEL01 from plasmid pRAT-4-A1.
PN   WO200208401-A2.
PD   31-JAN-2002.
PA   (ABBO ) ABBOTT LAB.
     Query Match             6.1%;
     Best Local Similarity   24.6%;   Score 73;   Pred. No. 17;   DB 5;   Length 272;

RESULT 950
ID   ADH80191 standard; protein; 272 AA.
DE   Fungal 7091 elongase protein seq id 75.
PN   US2003163845-A1.
PD   28-AUG-2003.
PA   (MUKE/) MUKERJI P.
PA   (LEON/) EUN-YEONG LEONARD A.
PA   (HUAN/) HUANG Y.
PA   (PERE/) PEREIRA S L.
     Query Match             6.1%;
     Best Local Similarity   19.9%;   Score 73;   Pred. No. 19;   DB 8;   Length 272;


RESULT 951
ID   ADW12982 standard; protein; 272 AA.
DE   Elongase protein #55.
PN   US2005009140-A1.
PD   13-JAN-2005.
PA   (MUKE/) MUKERJI P.
PA   (LEON/) LEONARD A E.
PA   (HUAN/) HUANG Y.
PA   (PERE/) PEREIRA S L.
     Query Match             6.1%;
     Best Local Similarity   19.9%;   Score 73;   Pred. No. 19;   DB 9;   Length 272;

RESULT 952
ID   ABM73154 standard; protein; 290 AA.
DE   Staphylococcus aureus protein #2394.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match             6.1%;
     Best Local Similarity   23.4%;   Score 73;   Pred. No. 20;   DB 6;   Length 290;

RESULT 953
ID   ABR47464 standard; protein; 322 AA.
DE   Breast cancer associated protein sequence SEQ ID NO:160.
PN   WO2003004989-A2.
PD   16-JAN-2003.
PA   (MILL-) MILLENIUM PHARM INC.
     Query Match             6.1%;
     Best Local Similarity   20.6%;   Score 73;   Pred. No. 24;   DB 6;   Length 322;

RESULT 954
ID   ADN61865 standard; protein; 349 AA.
DE   Human novel protein NOV42a.
PN   US2004043382-A1.
PD   04-MAR-2004.
PA   (PADI/) PADIGARU M.
PA   (SPYT/) SPYTEK K A.
PA   (SHEN/) SHENOY S G.
PA   (TAUP/) TAUPIER R J.
PA   (PENA/) PENA C E A.
PA   (LILL/) Li L.
PA   (ZERH/) ZERHUSEN B D.
PA   (GUSE/) GUSEV V Y.
PA   (JIWW/) JI W.
PA   (GORM/) GORMAN L.
PA   (MILL/) MILLER C E.
PA   (KEKU/) KEKUDA R.
PA   (PATT/) PATTURAJAN M.
PA   (GANG/) GANGOLLI E A.
PA   (VERN/) VERNET C A M.
PA   (GUOX/) GUO X S.
PA   (TCHE/) TCHERNEV V T.
PA   (FERN/) FERNANDES E R.
PA   (CASM/) CASMAN S J.
PA   (MALY/) MALYANKAR U M.
PA   (GERL/) GERLACH V.
PA   (LIUY/) LIU Y.
PA   (ANDE/) ANDERSON D W.
PA   (SPAD/) SPADERNA S K.
PA   (CATT/) CATTERTON E.
PA   (LEIT/) LEITE M W.
PA   (ZHON/) ZHONG H.
PA   (ALSO/) ALSOBROOK J P.
PA   (LEPL/) LEPLEY D M.
PA   (RIEG/) RIEGER D K.
PA   (BURG/) BURGESS C E.
     Query Match             6.1%;
     Best Local Similarity   24.0%;   Score 73;   Pred. No. 26;   DB 8;   Length 349;

RESULT 955
ID   AAW19613 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor type Ia.
PN   WO9722004-A1.
PD   19-JUN-1997.
PA   (MERI ) MERCK & CO INC.
     Query Match             6.1%;
     Best Local Similarity   6.1%;    Score 73;   Pred. No. 28;   DB 2;   Length 364;
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RESULT 956
ID   AAY54565 standard; protein; 364 AA.
DE   A mouse growth hormone secretagogue receptor.
PN   WO200002918-A1.
PD   20-JAN-2000.
PA   (MERI ) MERCK & CO INC.
     Query Match             6.1%;  Score 73;  DB 3;  Length 364;
     Best Local Similarity  19.4%;  Pred. No. 28;

RESULT 957
ID   AAB97377 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor (GHSR) related protein.
PN   WO200132705-A1.
PD   10-MAY-2001.
PA   (PRIM-) PRIMAL INC.
     Query Match             6.1%;  Score 73;  DB 8;  Length 364;
     Best Local Similarity  19.4%;  Pred. No. 28;

RESULT 958
ID   AD029026 standard; protein; 364 AA.
DE   Mouse novel GPCR GHSR, SEQ ID NO:125.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             6.1%;  Score 73;  DB 4;  Length 364;
     Best Local Similarity  19.4%;  Pred. No. 28;

RESULT 959
ID   AAW77773 standard; protein; 377 AA.
DE   Staphylococcus aureus protein of unknown function.
PN   EP841394-A2.
PD   13-MAY-1998.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
     Query Match             6.1%;  Score 73;  DB 2;  Length 377;
     Best Local Similarity  23.3%;  Pred. No. 29;

RESULT 960
ID   AAG50065 standard; protein; 415 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
     Query Match             6.1%;  Score 73;  DB 3;  Length 415;
     Best Local Similarity  19.8%;  Pred. No. 34;

RESULT 961
ID   AAG24013 standard; protein; 427 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 27528.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.1%;  Score 73;  DB 3;  Length 427;
     Best Local Similarity  22.0%;  Pred. No. 35;

RESULT 962
ID   AAG24012 standard; protein; 430 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.1%;  Score 73;  DB 3;  Length 430;
     Best Local Similarity  22.0%;  Pred. No. 35;

RESULT 963
ID   ABU31419 standard; protein; 453 AA.
DE   Protein encoded by Prokaryotic essential gene #16946.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.1%;  Score 73;  DB 6;  Length 453;
     Best Local Similarity  26.5%;  Pred. No. 38;

RESULT 964
ID   AEA16981 standard; protein; 469 AA.
DE   Arabidopsis thaliana protein #40.
PN   US200512515159-A1.
PD   09-JUN-2005.
PA   (CAOY/) CAO Y.
PA   (STEI/) STEIN J C.
     Query Match             6.1%;  Score 73;  DB 9;  Length 469;
     Best Local Similarity  19.8%;  Pred. No. 40;

RESULT 965
ID   AAG50064 standard; protein; 472 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.1%;  Score 73;  DB 3;  Length 472;
     Best Local Similarity  19.8%;  Pred. No. 40;

RESULT 966
ID   AAG50063 standard; protein; 474 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63402.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.1%;  Score 73;  DB 3;  Length 474;
     Best Local Similarity  19.8%;  Pred. No. 40;

RESULT 967
ID   ABM70313 standard; protein; 490 AA.
DE   Photorhabdus luminescens protein sequence #3410.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             6.1%;  Score 73;  DB 6;  Length 490;
     Best Local Similarity  24.6%;  Pred. No. 42;

RESULT 968
ID   AAY33766 standard; protein; 495 AA.
DE   hKv5.1 human brain-specific potassium channel.
PN   WO9941372-A1.
PD   19-AUG-1999.
PA   (ZENE ) ZENECA LTD.
     Query Match             6.1%;  Score 73;  DB 2;  Length 495;
     Best Local Similarity  23.2%;  Pred. No. 43;

RESULT 969
ID   ABO63300 standard; protein; 501 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9817.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match             6.1%;  Score 73;  DB 7;  Length 501;
     Best Local Similarity  23.3%;  Pred. No. 44;

RESULT 970
ID   ABP53583 standard; protein; 526 AA.
DE   Human NOV13b protein NOV50d.
PN   WO200262999-A2.
PD   15-AUG-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match             6.1%;  Score 73;  DB 5;  Length 526;
     Best Local Similarity  23.3%;  Pred. No. 47;

RESULT 971
ID   ADH42229 standard; protein; 526 AA.
DE   Novel human protein NOV50d.
PN   WO200310215159-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match             6.1%;  Score 73;  DB 8;  Length 526;
     Best Local Similarity  23.3%;  Pred. No. 47;

RESULT 972
ID   ABU31136 standard; protein; 553 AA.
DE   Protein encoded by Prokaryotic essential gene #16663.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.1%;  Score 73;  DB 6;  Length 553;
     Best Local Similarity  19.6%;  Pred. No. 50;

RESULT 973
ID   AAG24011 standard; protein; 556 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.1%;  Score 73;  DB 3;  Length 556;
     Best Local Similarity  22.0%;  Pred. No. 50;

RESULT 974
ID   ADQ96000 standard; protein; 608 AA.
DE   T cell activation associated protein #89.
PN   WO200405805-A2.
PD   15-JUL-2004.
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PA   (ASAHI-) ASAHI KASEI PHARMA CORP.
     Query Match          6.1%;   Score 73;   DB 8;   Length 608;
     Best Local Similarity     19.5%;   Pred. No. 57;
RESULT 975
ID   ADR99134 standard; protein; 635 AA.
DE   Human protein similar to yeast SSM4, TEB4, SEQ ID 140.
PN   WO2004078035-A2.
PD   16-SEP-2004.
PA   (FARB ) BAYER PHARM CORP.
     Query Match          6.1%;   Score 73;   DB 8;   Length 635;
     Best Local Similarity     19.5%;   Pred. No. 61;
RESULT 976
ID   ABB71311 standard; protein; 717 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 40725.
PN   WO200171042-A1.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match          6.1%;   Score 73;   DB 8;   Length 717;
     Best Local Similarity     21.3%;   Pred. No. 72;
RESULT 977
ID   AAW26673 standard; protein; 746 AA.
DE   Staphylococcus aureus spoIIIE protein.
PN   WO9726338-A1.
PD   24-JUL-1997.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
     Query Match          6.1%;   Score 73;   DB 4;   Length 746;
     Best Local Similarity     23.3%;   Pred. No. 76;
RESULT 978
ID   AAU37199 standard; protein; 748 AA.
DE   Staphylococcus aureus cellular proliferation protein #1369.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match          6.1%;   Score 73;   DB 2;   Length 748;
     Best Local Similarity     23.3%;   Pred. No. 76;
RESULT 979
ID   AAW88407 standard; protein; 750 AA.
DE   Human adult neural tissue secreted protein s195_10.
PN   WO9857976-A1.
PD   23-DEC-1998.
PA   (GEMY ) GENETICS INST INC.
     Query Match          6.1%;   Score 73;   DB 2;   Length 750;
     Best Local Similarity     19.5%;   Pred. No. 76;
RESULT 980
ID   AAW26672 standard; protein; 788 AA.
DE   Staphylococcus aureus spoIIIE protein.
PN   WO9726338-A1.
PD   24-JUL-1997.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
     Query Match          6.1%;   Score 73;   DB 4;   Length 788;
     Best Local Similarity     23.3%;   Pred. No. 82;
RESULT 981
ID   AAU36734 standard; protein; 788 AA.
DE   Staphylococcus aureus cellular proliferation protein #904.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match          6.1%;   Score 73;   DB 2;   Length 788;
     Best Local Similarity     23.3%;   Pred. No. 82;
RESULT 982
ID   ABU42392 standard; protein; 792 AA.
DE   Protein encoded by Prokaryotic essential gene #27919.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (GEMY ) GENETICS INST INC.
     Query Match          6.1%;   Score 73;   DB 2;   Length 792;
     Best Local Similarity     23.3%;   Pred. No. 82;
RESULT 983
ID   ABJ19057 standard; protein; 792 AA.
DE   Pathogen specific antigen related staphylococcal protein SEQ ID No 334.
PN   WO200259148-A2.
PD   01-AUG-2002.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
     Query Match          6.1%;   Score 73;   DB 6;   Length 792;
     Best Local Similarity     23.3%;   Pred. No. 82;
RESULT 984
ID   ABM73117 standard; protein; 792 AA.
DE   Staphylococcus aureus protein #2357.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match          6.1%;   Score 73;   DB 6;   Length 792;
     Best Local Similarity     23.3%;   Pred. No. 82;
RESULT 985
ID   AAW68466 standard; protein; 845 AA.
DE   Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
PN   WO9825960-A1.
PD   18-JUN-1998.
PA   (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
     Query Match          6.1%;   Score 73;   DB 2;   Length 845;
     Best Local Similarity     26.2%;   Pred. No. 90;
RESULT 986
ID   ADQ95946 standard; protein; 910 AA.
DE   T cell activation associated protein #62.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match          6.1%;   Score 73;   DB 2;   Length 910;
     Best Local Similarity     19.5%;   Pred. No. 1e+02;
RESULT 987
ID   ABG24246 standard; protein; 913 AA.
DE   Novel human diagnostic protein #24237.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match          6.1%;   Score 73;   DB 4;   Length 913;
     Best Local Similarity     21.3%;   Pred. No. 1e+02;
RESULT 988
ID   AAM51861 standard; protein; 966 AA.
DE   Murine polycystic kidney disease protein 2.
PN   WO200177331-A1.
PD   18-OCT-2001.
PA   (MILL-) MILLENIUM PHARM INC.
     Query Match          6.1%;   Score 73;   DB 5;   Length 966;
     Best Local Similarity     21.3%;   Pred. No. 1.1e+02;
RESULT 989
ID   ABB07819 standard; protein; 966 AA.
DE   Mouse polycystic kidney disease protein 2.
PN   US2002035056-A1.
PD   21-MAR-2002.
PA   (CURT/) CURTIS R A J.
PA   (SILO/) SILOS-SANTIAGO I.
     Query Match          6.1%;   Score 73;   DB 8;   Length 966;
     Best Local Similarity     21.3%;   Pred. No. 1.1e+02;
RESULT 990
ID   ADJ76159 standard; protein; 966 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:1411.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
     Query Match          6.1%;   Score 73;   DB 5;   Length 966;
     Best Local Similarity     21.3%;   Pred. No. 1.1e+02;
RESULT 991
ID   ADV66235 standard; protein; 966 AA.
DE   Polycystic kidney disease protein 2, SEQ ID 11.
PN   US2004248160-A1.
PD   09-DEC-2004.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          6.1%;   Score 73;   DB 9;   Length 966;
     Best Local Similarity     21.3%;   Pred. No. 1.1e+02;
RESULT 992
ID   ADZ26335 standard; protein; 966 AA.
DE   Human hypoxia-responsive protein CNGH0002.1.
PN   WO2005033293-A2.
PD   14-APR-2005.
PA   (CENZ ) CENTOCOR INC.
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RESULT 993
  Query Match        6.1%;    Score 73;    DB 9;   Length 966;
  Best Local Similarity   19.5%;   Pred. No. 1.1e+02;
ID  ABG05866 standard; protein; 971 AA.
DE  Novel human diagnostic protein #5857.
PN  WO200175067-A2.
PD  11-OCT-2001.
PA  (HYSE-) HYSEQ INC.

RESULT 994
  Query Match        6.1%;    Score 73;    DB 4;   Length 971;
  Best Local Similarity   19.5%;   Pred. No. 1.1e+02;
ID  ADR99135 standard; protein; 971 AA.
DE  Human protein similar to yeast SSM4, TEB4, SEQ ID 141.
PN  WO200478035-A2.
PD  16-SEP-2004.
PA  (FARB ) BAYER PHARM CORP.

RESULT 995
  Query Match        6.1%;    Score 73;    DB 9;   Length 971;
  Best Local Similarity   19.5%;   Pred. No. 1.1e+02;
ID  AD211480 standard; protein; 971 AA.
DE  MARCH VI protein, SEQ ID 49.
PN  US200507961-A1.
PD  14-APR-2005.
PA  (UYOR-) UNIV OREGON HEALTH SCI.

RESULT 996
  Query Match        6.1%;    Score 73;    DB 9;   Length 971;
  Best Local Similarity   19.5%;   Pred. No. 1.1e+02;
ID  AD211490 standard; protein; 971 AA.
DE  MARCH VI protein, SEQ ID 59.
PN  US200507961-A1.
PD  14-APR-2005.
PA  (UYOR-) UNIV OREGON HEALTH SCI.

RESULT 997
  Query Match        6.1%;    Score 73;    DB 8;   Length 971;
  Best Local Similarity   19.5%;   Pred. No. 1.1e+02;
ID  ABG07373 standard; protein; 976 AA.
DE  Novel human diagnostic protein #7364.
PN  WO200175067-A2.
PD  11-OCT-2001.
PA  (HYSE-) HYSEQ INC.

RESULT 998
  Query Match        6.1%;    Score 73;    DB 9;   Length 3010;
  Best Local Similarity   19.5%;   Pred. No. 1.1e+02;
ID  ADX40795 standard; protein; 3010 AA.
DE  HCV polymerase protein #18.
PN  WO200512502-A2.
PD  10-FEB-2005.
PA  (EPIM-) EPIMMUNE INC.

RESULT 999
  Query Match        6.1%;    Score 73;    DB 9;   Length 3010;
  Best Local Similarity   26.2%;   Pred. No. 5.3e+02;
ID  ABU05456 standard; protein; 209 AA.
DE  M.tuberculosis and M.leprae marker protein #107.
PN  WO200274903-A2.
PD  26-SEP-2002.
PA  (INSP ) INST PASTEUR.

RESULT 1000
  Query Match        6.1%;    Score 72.5;   DB 5;   Length 209;
  Best Local Similarity   22.1%;   Pred. No. 15;
ID  ABU15302 standard; protein; 222 AA.
DE  Protein encoded by Prokaryotic essential gene #829.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.

RESULT 1001
  Query Match        6.1%;    Score 72.5;   DB 6;   Length 222;
  Best Local Similarity   20.5%;   Pred. No. 16;
ID  ADY24595 standard; protein; 274 AA.
DE  Plant full length insert polypeptide seqid 72379.
PN  US200403488-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
PA  (KOVA/) KOVALIC D K.
PA  (SCRE/) SCREEN S E.
PA  (TABA/) TABASKA J E.
PA  (CAOY/) CAO Y.

RESULT 1002
  Query Match        6.1%;    Score 72.5;   DB 8;   Length 274;
  Best Local Similarity   26.5%;   Pred. No. 22;
ID  ADX95386 standard; protein; 274 AA.
DE  Plant full length insert polypeptide seqid 58050.
PN  US200403488-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
PA  (KOVA/) KOVALIC D K.
PA  (SCRE/) SCREEN S E.
PA  (TABA/) TABASKA J E.
PA  (CAOY/) CAO Y.

RESULT 1003
  Query Match        6.1%;    Score 72.5;   DB 5;   Length 307;
  Best Local Similarity   22.9%;   Pred. No. 25;
ID  ABB53879 standard; protein; 307 AA.
DE  Lactococcus lactis protein yfgG.
PN  FR2807446-A1.
PD  12-OCT-2001.
PA  (INRG ) INRA INST NAT RECH AGRONOMIQUE.

RESULT 1004
  Query Match        6.1%;    Score 72.5;   DB 8;   Length 307;
  Best Local Similarity   25.3%;   Pred. No. 25;
ID  ADY10668 standard; protein; 307 AA.
DE  Plant full length insert polypeptide seqid 66483.
PN  US200403488-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
PA  (KOVA/) KOVALIC D K.
PA  (SCRE/) SCREEN S E.
PA  (TABA/) TABASKA J E.
PA  (CAOY/) CAO Y.

RESULT 1005
  Query Match        6.1%;    Score 72.5;   DB 8;   Length 307;
  Best Local Similarity   25.3%;   Pred. No. 25;
ID  ADY11265 standard; protein; 307 AA.
DE  Plant full length insert polypeptide seqid 67080.
PN  US200403488-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
PA  (KOVA/) KOVALIC D K.
PA  (SCRE/) SCREEN S E.
PA  (TABA/) TABASKA J E.
PA  (CAOY/) CAO Y.

RESULT 1006
  Query Match        6.1%;    Score 72.5;   DB 8;   Length 307;
  Best Local Similarity   25.3%;   Pred. No. 25;
ID  ADY10993 standard; protein; 307 AA.
DE  Plant full length insert polypeptide seqid 66808.
PN  US200403488-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
PA  (KOVA/) KOVALIC D K.
PA  (SCRE/) SCREEN S E.
PA  (TABA/) TABASKA J E.
PA  (CAOY/) CAO Y.

RESULT 1007
  Query Match        6.1%;    Score 72.5;   DB 8;   Length 307;
  Best Local Similarity   25.3%;   Pred. No. 25;
ID  ADY11014 standard; protein; 308 AA.
DE  Plant full length insert polypeptide seqid 66829.
PN  US200403488-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
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PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 8;   Length 308;
                        25.3%;   Pred. No. 25;

RESULT 1008
ID ADY10930 standard; protein; 310 AA.
DE Plant full length insert polypeptide seqid 66745.
PN US20040348888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 8;   Length 310;
                        25.3%;   Pred. No. 26;

RESULT 1009
ID ADY11546 standard; protein; 310 AA.
DE Plant full length insert polypeptide seqid 67361.
PN US20040348888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 8;   Length 310;
                        25.3%;   Pred. No. 26;

RESULT 1010
ID ADY09462 standard; protein; 311 AA.
DE Plant full length insert polypeptide seqid 65277.
PN US20040348888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 8;   Length 311;
                        25.3%;   Pred. No. 26;

RESULT 1011
ID ADY11115 standard; protein; 312 AA.
DE Plant full length insert polypeptide seqid 66930.
PN US20040348888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 8;   Length 312;
                        25.3%;   Pred. No. 26;

RESULT 1012
ID ADY10946 standard; protein; 312 AA.
DE Plant full length insert polypeptide seqid 66761.
PN US20040348888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 8;   Length 312;
                        25.3%;   Pred. No. 26;

RESULT 1013
ID ABB53675 standard; protein; 325 AA.

DE Lactococcus lactis protein ydhB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 5;   Length 325;
                        25.9%;   Pred. No. 27;

RESULT 1014
ID ADH87677 standard; protein; 353 AA.
DE Enterococcus faecalis polypeptide #2157.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 7;   Length 353;
                        21.5%;   Pred. No. 31;

RESULT 1015
ID ADH87557 standard; protein; 359 AA.
DE Enterococcus faecalis polypeptide #2037.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 7;   Length 359;
                        25.0%;   Pred. No. 31;

RESULT 1016
ID AAR37264 standard; protein; 389 AA.
DE Oxytocin receptor.
PN EP542424-A1.
PD 19-MAY-1993.
PA (ROHT) ROHTO PHARM CO LTD.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 2;   Length 389;
                        24.5%;   Pred. No. 35;

RESULT 1017
ID AAW23832 standard; protein; 389 AA.
DE Human oxytocin receptor.
PN EP811684-A2.
PD 10-DEC-1997.
PA (ROHT) ROHTO PHARM CO LTD.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 2;   Length 389;
                        24.5%;   Pred. No. 35;

RESULT 1018
ID AAM40217 standard; protein; 389 AA.
DE Human polypeptide SEQ ID NO 3362.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 4;   Length 389;
                        24.5%;   Pred. No. 35;

RESULT 1019
ID ABP81865 standard; protein; 389 AA.
DE Human oxytocin receptor protein SEQ ID NO:215.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 6;   Length 389;
                        24.5%;   Pred. No. 35;

RESULT 1020
ID AAE38317 standard; protein; 389 AA.
DE Human oxytocin receptor protein.
PN WO2003064402-A1.
PD 07-AUG-2003.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 6;   Length 389;
                        24.5%;   Pred. No. 35;

RESULT 1021
ID ADF12125 standard; protein; 389 AA.
DE Human oxytocin receptor protein (OXTR) protein SEQ ID NO:2.
PN WO2003093816-A2.
PD 13-NOV-2003.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity   6.1%;   Score 72.5;   DB 8;   Length 389;
                        24.5%;   Pred. No. 35;

RESULT 1022
ID   ADI03915 standard; protein; 389 AA.
DE   Human oxytocin receptor polypeptide.
PA   (UXQU-) UNIV QUEBEC A MONTREAL.
PA   (UYMO-) UNIV MONTREAL CENT HOSPITALIER.
PN   WO200400993-A2.
PN   WO200400000-A2.
PD   31-DEC-2003.
PA   (PRIM-) PRIMAL INC.
PD   13-MAY-2004.
  Query Match 6.1%; Score 72.5; Pred. No. 35; DB 8; Length 389;
Best Local Similarity 24.5%;

RESULT 1023
ID   ADO29590 standard; protein; 389 AA.
DE   Human GPCR OXTR, SEQ ID NO:692.
PA   (ASTR) ASTRAZENECA AB.
PA   (ASTR) ASTRAZENECA UK LTD.
PN   US2005012565-A1.
PD   10-FEB-2005.
  Query Match 6.1%; Score 72.5; Pred. No. 35; DB 8; Length 389;
Best Local Similarity 24.5%;

RESULT 1024
ID   ADW98687 standard; protein; 389 AA.
DE   Human oxytocin receptor (OXTR) protein SeqID1.
PA   (INSP) INST PASTEUR.
  Query Match 6.1%; Score 72.5; Pred. No. 35; DB 9; Length 389;
Best Local Similarity 24.5%;

RESULT 1025
ID   AAR58665 standard; protein; 448 AA.
DE   Bovine PACAP receptor type 1B mature protein.
PA   (TAKE) TAKEDA CHEM IND LTD.
PN   EP618291-A2.
PD   05-OCT-1994.
  Query Match 6.1%; Score 72.5; Pred. No. 43; DB 2; Length 448;
Best Local Similarity 29.6%;

RESULT 1026
ID   AAR58663 standard; protein; 476 AA.
DE   Bovine PACAP receptor type 1A mature protein.
PA   (TAKE) TAKEDA CHEM IND LTD.
PN   EP618291-A2.
PD   05-OCT-1994.
  Query Match 6.1%; Score 72.5; Pred. No. 47; DB 2; Length 476;
Best Local Similarity 29.6%;

RESULT 1027
ID   AAR58657 standard; protein; 485 AA.
DE   Bovine PACAP receptor type 1B protein.
PA   (TAKE) TAKEDA CHEM IND LTD.
PN   EP618291-A2.
PD   05-OCT-1994.
  Query Match 6.1%; Score 72.5; Pred. No. 48; DB 2; Length 485;
Best Local Similarity 29.6%;

RESULT 1028
ID   AAR58655 standard; protein; 513 AA.
DE   Bovine PACAP receptor type 1A protein.
PA   (TAKE) TAKEDA CHEM IND LTD.
PN   EP618291-A2.
PD   05-OCT-1994.
  Query Match 6.1%; Score 72.5; Pred. No. 52; DB 2; Length 513;
Best Local Similarity 29.6%;

RESULT 1029
ID   ADN19765 standard; protein; 522 AA.
DE   Bacterial polypeptide #2418.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
PN   US2003233675-A1.
PD   18-DEC-2003.
  Query Match 6.1%; Score 72.5; Pred. No. 53; DB 8; Length 522;
Best Local Similarity 22.5%;

RESULT 1030
ID   ADV89115 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein sequence, SEQ ID 1509.
PN   FR2824074-A1.
PD   31-OCT-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
  Query Match 6.1%; Score 72.5; Pred. No. 74; DB 8; Length 666;
Best Local Similarity 23.1%;

RESULT 1031
ID   ADV82479 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein, SEQ ID 3620.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
PN   WO200292818-A2.
PD   21-NOV-2002.
  Query Match 6.1%; Score 72.5; Pred. No. 74; DB 8; Length 666;
Best Local Similarity 23.1%;

RESULT 1032
ID   ADV80368 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein, SEQ ID 1509.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
PN   WO200292818-A2.
PD   21-NOV-2002.
  Query Match 6.1%; Score 72.5; Pred. No. 74; DB 8; Length 666;
Best Local Similarity 23.1%;

RESULT 1033
ID   ADI81620 standard; protein; 769 AA.
DE   C. elegans protein similar to Pfam PF00023.
PA   (REGC) ROOS J.
PA   (ROOS/) ROOS J.
PA   (STAU/) STAUDERMAN K.
PA   (VEII/) VELICELEBI G.
PN   US200400959537-A1.
PN   WO200196585-A2.
PD   15-JAN-2004.
PD   20-DEC-2001.
  Query Match 6.1%; Score 72.5; Pred. No. 91; DB 8; Length 769;
Best Local Similarity 20.2%;

RESULT 1034
ID   ABB05429 standard; protein; 848 AA.
DE   Arabidopsis thaliana ABHI protein SEQ ID NO:2.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
PN   WO200281696-A2.
PD   17-OCT-2002.
  Query Match 6.1%; Score 72.5; Pred. No. 1e+02; DB 6; Length 848;
Best Local Similarity 22.3%;

RESULT 1035
ID   AAE31528 standard; protein; 848 AA.
DE   Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
PA   (REGC) UNIV CALIFORNIA.
PN   WO200277183-A2.
PD   03-OCT-2002.
  Query Match 6.1%; Score 72.5; Pred. No. 1e+02; DB 5; Length 848;
Best Local Similarity 22.3%;

RESULT 1036
ID   ABU25159 standard; protein; 851 AA.
DE   Protein encoded by Prokaryotic essential gene #10686.
PA   (ELIT-) ELITRA PHARM INC.
PN   US2004034888-A1.
PD   19-FEB-2004.
  Query Match 6.1%; Score 72.5; Pred. No. 1e+02; DB 6; Length 851;
Best Local Similarity 20.5%;

RESULT 1037
ID   ADY10144 standard; protein; 903 AA.
DE   Plant full length insert polypeptide seqid 65959.
PA   (CAOY/) CAO Y.
PN   US2004034888-A1.
PD   18-FEB-2004.
  Query Match 6.1%; Score 72.5; Pred. No. 1.1e-02; DB 8; Length 903;
Best Local Similarity 20.5%;

RESULT 1038
ID   ADW76078 standard; protein; 1051 AA.
DE   Streptococcus agalactiae protein; 1051 AA.

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DE   Human cytomegalovirus (HCMV) pp65-IE1 fusion protein.
PN   WO200507689-A1.
PD   27-JAN-2005.
PA   (ALPH-) ALPHAVAX INC.
     Query Match             6.1%;
     Best Local Similarity   19.3%;
     Score 72.5; DB 9; Length 1051;
     Pred. No. 1.4e+02;

RESULT 1039
ID   AAR34580 standard; protein; 3010 AA.
DE   Human hepatitis C virus gene encoded polypeptide.
PN   EP541089-A2.
PD   12-MAY-1993.
PA   (SANW ) SANWA KAGAKU KENKYUSHO CO.
     Query Match             6.1%;
     Best Local Similarity   23.7%;
     Score 72.5; DB 2; Length 3010;
     Pred. No. 6e+02;

RESULT 1040
ID   ADQ96378 standard; protein; 208 AA.
DE   T cell activation associated protein #278.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match             6.0%;
     Best Local Similarity   20.8%;
     Score 72; DB 8; Length 208;
     Pred. No. 17;

RESULT 1041
ID   ABB48543 standard; protein; 306 AA.
DE   Listeria monocytogenes protein #1247.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST PASTEUR.
     Query Match             6.0%;
     Best Local Similarity   21.0%;
     Score 72; DB 5; Length 306;
     Pred. No. 29;

RESULT 1042
ID   ABU39432 standard; protein; 317 AA.
DE   Protein encoded by Prokaryotic essential gene #24959.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             6.0%;
     Best Local Similarity   28.8%;
     Score 72; DB 3; Length 317;
     Pred. No. 30;

RESULT 1043
ID   AAB53392 standard; protein; 334 AA.
DE   Human colon cancer antigen protein sequence SEQ ID NO:932.
PN   WO200055351-A1.
PD   21-SEP-2000.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.0%;
     Best Local Similarity   23.5%;
     Score 72; DB 3; Length 334;
     Pred. No. 33;

RESULT 1044
ID   AAV87505 standard; protein; 370 AA.
DE   Human G coupled-protein receptor; hGR3.
PN   WO200017641-A1.
PD   30-MAR-2000.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match             6.0%;
     Best Local Similarity   21.8%;
     Score 72; DB 3; Length 370;
     Pred. No. 38;

RESULT 1045
ID   AAW20731 standard; protein; 375 AA.
DE   H. Pylori inner membrane protein, 06cp1111l8orf6.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR ) ASTRA AB.
     Query Match             6.0%;
     Best Local Similarity   20.9%;
     Score 72; DB 2; Length 375;
     Pred. No. 38;

RESULT 1046
ID   ABU19932 standard; protein; 396 AA.
DE   Protein encoded by Prokaryotic essential gene #5459.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.0%;
     Best Local Similarity   21.6%;
     Score 72; DB 6; Length 396;
     Pred. No. 41;

RESULT 1047
ID   ABG25051 standard; protein; 414 AA.
DE   Novel human diagnostic protein #25042.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             6.0%;
     Best Local Similarity   22.6%;
     Score 72; DB 4; Length 414;
     Pred. No. 44;

RESULT 1048
ID   AAG50203 standard; protein; 427 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.0%;
     Best Local Similarity   22.0%;
     Score 72; DB 3; Length 427;
     Pred. No. 46;

RESULT 1049
ID   AAG50202 standard; protein; 430 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.0%;
     Best Local Similarity   22.0%;
     Score 72; DB 3; Length 430;
     Pred. No. 46;

RESULT 1050
ID   ABM72825 standard; protein; 447 AA.
DE   Staphylococcus aureus protein #2065.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match             6.0%;
     Best Local Similarity   23.9%;
     Score 72; DB 6; Length 447;
     Pred. No. 49;

RESULT 1051
ID   ABB62902 standard; protein; 448 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 15498.
PN   WO200171042-A2.
PD   27-SEP-2002.
PA   (PEKE ) PE CORP NY.
     Query Match             6.0%;
     Best Local Similarity   25.1%;
     Score 72; DB 4; Length 448;
     Pred. No. 49;

RESULT 1052
ID   ABJ18913 standard; protein; 453 AA.
DE   Pathogen specific antigen related staphylococcal protein SEQ ID No 59.
PN   WO200259148-A2.
PD   01-AUG-2002.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
     Query Match             6.0%;
     Best Local Similarity   23.9%;
     Score 72; DB 6; Length 453;
     Pred. No. 50;

RESULT 1053
ID   ABU16441 standard; protein; 453 AA.
DE   Protein encoded by Prokaryotic essential gene #1968.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.0%;
     Best Local Similarity   23.9%;
     Score 72; DB 6; Length 453;
     Pred. No. 50;

RESULT 1054
ID   ADN73057 standard; protein; 468 AA.
DE   Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
PN   WO2004035798-A2.
PD   29-APR-2004.
PA   (CROP-) CROPDESIGN NV.
     Query Match             6.0%;
     Best Local Similarity   21.8%;
     Score 72; DB 8; Length 468;
     Pred. No. 52;

RESULT 1055
ID   AAG16338 standard; protein; 495 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.0%;
     Best Local Similarity   21.8%;
     Score 72; DB 3; Length 495;
     Pred. No. 56;

RESULT 1056
ID   AAG16337 standard; protein; 497 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.0%;
     Best Local Similarity   21.3%;
     Score 72; DB 3; Length 497;
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RESULT 1057
ID   AAG16336 standard; protein; 507 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.0%;
     Best Local Similarity  21.3%;
     Score 72; DB 3; Pred. No. 58; Length 507;

RESULT 1058
ID   ADS23568 standard; protein; 543 AA.
DE   Bacterial polypeptide #12601.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD//) GOLDMAN B S.
     Query Match             6.0%;
     Best Local Similarity  18.6%;
     Score 72; DB 8; Pred. No. 64; Length 543;

RESULT 1059
ID   ABU25738 standard; protein; 552 AA.
DE   Protein encoded by Prokaryotic essential gene #11265.
PN   WO200277183-A2.
PD   03-OCT-2002.
     Query Match             6.0%;
     Best Local Similarity  19.5%;
     Score 72; DB 6; Pred. No. 65; Length 552;

RESULT 1060
ID   AAG50201 standard; protein; 556 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
PN   WO200294867-A2.
PD   28-NOV-2002.
     Query Match             6.0%;
     Best Local Similarity  18.6%;
     Score 72; DB 3; Pred. No. 66; Length 556;

RESULT 1061
ID   ADJ69383 standard; protein; 594 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1189.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (BUCK-) BUCK INST AGE RES.
PA   (MITO-) MITOKOR.
     Query Match             6.0%;
     Best Local Similarity  22.0%;
     Score 72; DB 7; Pred. No. 73; Length 594;

RESULT 1062
ID   ABP97202 standard; protein; 696 AA.
DE   Tumour-associated antigenic target protein TAT247 SEQ ID NO:84.
PN   WO200302492-A2.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             6.0%;
     Best Local Similarity  20.8%;
     Score 72; DB 6; Pred. No. 90; Length 696;

RESULT 1063
ID   ABP97201 standard; protein; 696 AA.
DE   Tumour-associated antigenic target protein TAT225 SEQ ID NO:83.
PN   WO2003024392-A2.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             6.0%;
     Best Local Similarity  20.8%;
     Score 72; DB 6; Pred. No. 90; Length 696;

RESULT 1064
ID   ABP81969 standard; protein; 696 AA.
DE   Human GPCR XPR1 protein SEQ ID NO:424.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match             6.0%;
     Best Local Similarity  20.8%;
     Score 72; DB 6; Pred. No. 90; Length 696;

RESULT 1065
ID   ADB67652 standard; protein; 696 AA.
DE   Human xenotropic polytropic retrovirus receptor, SEQ ID 21.
PN   WO2003072824-A1.
PD   04-SEP-2003.
PA   (SANY ) SANKYO CO LTD.
     Query Match             6.0%;
     Best Local Similarity  20.8%;
     Score 72; DB 3; Pred. No. 90; Length 696;

RESULT 1066
ID   ADQ96380 standard; protein; 696 AA.
DE   T cell activation associated protein #279.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match             6.0%;
     Best Local Similarity  20.8%;
     Score 72; DB 7; Pred. No. 90; Length 696;

RESULT 1067
ID   ABM69179 standard; protein; 724 AA.
DE   Photorhabdus luminescens protein sequence #2276.
PN   WO200294867-A2.
PD   28-NOV-2002.
     Query Match             6.0%;
     Best Local Similarity  21.3%;
     Score 72; DB 8; Pred. No. 95; Length 724;

RESULT 1068
ID   AAB46702 standard; protein; 741 AA.
DE   P. falciparum DNA polymerase protein fragment SEQ ID NO 11.
PN   WO200075335-A2.
PD   14-DEC-2000.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             6.0%;
     Best Local Similarity  21.3%;
     Score 72; DB 6; Pred. No. 99; Length 741;

RESULT 1069
ID   AAM47977 standard; protein; 788 AA.
DE   Human hARRG.
PN   CN1115342-A.
PD   03-OCT-2001.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             6.0%;
     Best Local Similarity  30.4%;
     Score 72; DB 4; Pred. No. 1.1e+02; Length 788;

RESULT 1070
ID   AAB58917 standard; protein; 1275 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 3543.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
PA   (PEKE ) PE CORP NY.
     Query Match             6.0%;
     Best Local Similarity  26.3%;
     Score 72; DB 5; Pred. No. 2.1e+02; Length 1275;

RESULT 1071
ID   AAY70064 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-1 polyprotein.
PN   WO200008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match             6.0%;
     Best Local Similarity  19.0%;
     Score 72; DB 3; Pred. No. 4.8e+02; Length 2307;

RESULT 1072
ID   AAY70065 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-3 polyprotein.
PN   WO200008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match             6.0%;
     Best Local Similarity  23.6%;
     Score 72; DB 3; Pred. No. 4.8e+02; Length 2307;

RESULT 1073
ID   AAY70066 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-4 polyprotein.
PN   WO200008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match             6.0%;
     Best Local Similarity  23.6%;
     Score 72; DB 3; Pred. No. 4.8e+02; Length 2307;

RESULT 1074
ID   AAM93791 standard; protein; 208 AA.
DE   Human polypeptide, SEQ ID NO: 3817.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
     Query Match             6.0%;
     Best Local Similarity  23.6%;
     Score 72; DB 3; Pred. No. 4.8e+02; Length 208;
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RESULT 1075
ID   ADL31784 standard; protein; 208 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3817.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match
  Best Local Similarity   25.2%;
  Score 71.5;  DB 4;  Length 208;

RESULT 1076
ID   AAG56417 standard; protein; 209 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match
  Best Local Similarity   25.6%;
  Score 71.5;  DB 3;  Length 209;

RESULT 1077
ID   AAG56416 standard; protein; 216 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match
  Best Local Similarity   25.6%;
  Score 71.5;  DB 3;  Length 216;

RESULT 1078
ID   AAG16922 standard; protein; 218 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match
  Best Local Similarity   42.4%;
  Score 71.5;  DB 3;  Length 218;

RESULT 1079
ID   ABB53486 standard; protein; 301 AA.
DE   Lactococcus lactis protein ybiG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG-) INRA INST NAT RECH AGRONOMIQUE.
  Query Match
  Best Local Similarity   26.5%;
  Score 71.5;  DB 5;  Length 301;

RESULT 1080
ID   AAW37976 standard; protein; 342 AA.
DE   Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
PN   WO9815289-A1.
PD   16-APR-1998.
PA   (CORR-) CORNELL RES FOUND INC.
  Query Match
  Best Local Similarity   22.2%;
  Score 71.5;  DB 2;  Length 342;

RESULT 1081
ID   ADG87423 standard; protein; 348 AA.
DE   Meloidogyne incognita plk1 protein.
PN   US2003150017-A1.
PD   07-AUG-2003.
PA   (GRAH/) GRAHAM M W.
PA   (FAIR/) FAIRBAIRN D J.
  Query Match
  Best Local Similarity   21.0%;
  Score 71.5;  DB 7;  Length 348;

RESULT 1082
ID   ADR40542 standard; protein; 363 AA.
DE   Ovine Mr1a protein.
PN   US20040161623-A1.
PD   19-AUG-2004.
PA   (MESA/) MESA J R B.
  Query Match
  Best Local Similarity   21.0%;
  Score 71.5;  DB 8;  Length 363;

RESULT 1083
ID   AAR88410 standard; protein; 366 AA.
DE   High-affinity melatonin-1a receptor.
PN   WO9535320-A1.
PD   28-DEC-1995.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
  Query Match
  Best Local Similarity   23.1%;
  Score 71.5;  DB 7;  Length 366;

RESULT 1084
ID   ABU03456 standard; protein; 382 AA.
DE   Angiogenesis-associated human protein sequence #1.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
  Query Match
  Best Local Similarity   23.1%;
  Score 71.9;  DB 2;  Length 366;

RESULT 1085
ID   ABP58069 standard; protein; 382 AA.
DE   Human G-protein coupled receptor GAVE1.
PN   WO200295056-A2.
PD   28-NOV-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match
  Best Local Similarity   22.3%;
  Score 71.5;  DB 6;  Length 382;

RESULT 1086
ID   ABP59277 standard; protein; 382 AA.
DE   Human Edg1 receptor.
PN   WO200306503-A1.
PD   23-JAN-2003.
PA   (AVET-) AVENTIS PHARM INC.
  Query Match
  Best Local Similarity   22.3%;
  Score 71.5;  DB 6;  Length 382;

RESULT 1087
ID   ABU08809 standard; protein; 382 AA.
DE   Human EDG-1 protein.
PN   US2002155512-A1.
PD   24-OCT-2002.
PA   (CERB-) CERETEK.
  Query Match
  Best Local Similarity   22.3%;
  Score 71.5;  DB 6;  Length 382;

RESULT 1088
ID   ABR59701 standard; protein; 382 AA.
DE   Human endothelial differentiation sphingolipid GPCR 1.
PN   WO2003029277-A2.
PD   10-APR-2003.
PA   (RIGE-) RIGEL PHARM INC.
  Query Match
  Best Local Similarity   22.3%;
  Score 71.5;  DB 6;  Length 382;

RESULT 1089
ID   ABP81876 standard; protein; 382 AA.
DE   Human sphingolipid receptor Edg1 protein SEQ ID NO:237.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
  Query Match
  Best Local Similarity   22.3%;
  Score 71.5;  DB 6;  Length 382;

RESULT 1090
ID   ADB67662 standard; protein; 382 AA.
DE   Human EDG1, SEQ ID 31.
PN   WO200307824-A1.
PD   04-SEP-2003.
PA   (SANY-) SANKYO CO LTD.
  Query Match
  Best Local Similarity   22.3%;
  Score 71.5;  DB 7;  Length 382;

RESULT 1091
ID   ADC40477 standard; protein; 382 AA.
DE   Protein of human EDG-1.
PN   WO200305096-A1.
PD   26-JUN-2003.
PA   (TAKE-) TAKEDA CHEM IND LTD.
  Query Match
  Best Local Similarity   22.3%;
  Score 71.5;  DB 7;  Length 382;

RESULT 1092
ID   ADN38684 standard; protein; 382 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:2.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match
  Best Local Similarity   22.3%;
  Score 71.5;  DB 7;  Length 382;
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Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 7;   Length 382;
                        22.3%; Pred. No. 45;
RESULT 1093
ID ABM85457 standard; protein; 382 AA.
DE Human protein sequence hCP1630135.
PN WO200307826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 7;   Length 382;
                        22.3%; Pred. No. 45;
RESULT 1094
ID ADJ45541 standard; protein; 382 AA.
DE LXR-ligand induced transcript seq id 72.
PN US2004023276-A1.
PD 05-FEB-2004.
PA (WARD/) WARD T R.
PA (MAOM/) MAO M.
PA (LINS/) LINSLEY P S.
PA (LUND/) LUND E.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 8;   Length 382;
                        22.3%; Pred. No. 45;
RESULT 1095
ID ADR67022 standard; protein; 382 AA.
DE Human cancer associated protein sequence SEQ ID NO:68.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 8;   Length 382;
                        22.3%; Pred. No. 45;
RESULT 1096
ID ADY19566 standard; protein; 382 AA.
DE PRO polypeptide SEQ ID NO 5372.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 9;   Length 382;
                        22.3%; Pred. No. 45;
RESULT 1097
ID ADZ12975 standard; protein; 382 AA.
DE Human cancer-associated protein #147.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 9;   Length 382;
                        22.3%; Pred. No. 45;
RESULT 1098
ID ADZ12973 standard; protein; 382 AA.
DE Human cancer-associated protein #146.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 9;   Length 382;
                        22.3%; Pred. No. 45;
RESULT 1099
ID ADN19614 standard; protein; 383 AA.
DE Bacterial polypeptide #2267.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 8;   Length 383;
                        22.0%; Pred. No. 45;
RESULT 1100
ID ABB05226 standard; protein; 390 AA.
DE Catostomus commersoni isotocin receptor protein SEQ ID NO:3.
PN WO20019296-A2.
PD 06-DEC-2001.
PA (FARB) BAYER AG.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 5;   Length 390;
                        22.2%; Pred. No. 46;

RESULT 1101
ID ADM83141 standard; protein; 394 AA.
DE Rat vesicle membrane protein (VMP)2.
PN US200315787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 7;   Length 394;
                        21.4%; Pred. No. 47;
RESULT 1102
ID AB848023 standard; protein; 435 AA.
DE Listeria monocytogenes protein #727.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 5;   Length 435;
                        22.7%; Pred. No. 54;
RESULT 1103
ID AAR22000 standard; protein; 441 AA.
DE Partial M17 antigen from Region II, encoded by PCR prod.
PN WO9203457-A.
PD 05-MAR-1992.
PA (REGC) UNIV CALIFORNIA.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 2;   Length 441;
                        22.6%; Pred. No. 55;
RESULT 1104
ID ADX93096 standard; protein; 448 AA.
DE Plant full length insert polypeptide seqid 55760.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 8;   Length 448;
                        22.3%; Pred. No. 56;
RESULT 1105
ID ABP75877 standard; protein; 470 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1061.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 6;   Length 470;
                        22.4%; Pred. No. 60;
RESULT 1106
ID ABU26033 standard; protein; 524 AA.
DE Protein encoded by Prokaryotic essential gene #11560.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 6;   Length 524;
                        26.6%; Pred. No. 70;
RESULT 1107
ID ABJ37074 standard; protein; 565 AA.
DE Human breast cancer / ovarian cancer related protein #50.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 6;   Length 565;
                        22.4%; Pred. No. 77;
RESULT 1108
ID AAW51244 standard; protein; 568 AA.
DE Human calcitonin receptor.
PN WO9821242-A1.
PD 22-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 2;   Length 568;
                        22.4%; Pred. No. 78;
RESULT 1109
ID ABU16392 standard; protein; 603 AA.
DE Protein encoded by Prokaryotic essential gene #1919.
PN WO200271183-A2.

PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.0%; Score 71.5; DB 6; Length 603;
     Best Local Similarity   21.3%; Pred. No. 85;
ID   ABM72619 standard; protein; 603 AA.
DE   Staphylococcus aureus protein #1855.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match   6.0%; Score 71.5; DB 6; Length 603;
     Best Local Similarity   21.3%; Pred. No. 85;
RESULT 1111
ID   ADM43215 standard; protein; 697 AA.
DE   Human methionine synthase reductase del Arg 559 variant.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; Score 71.5; DB 7; Length 697;
     Best Local Similarity   22.8%; Pred. No. 1e+02;
RESULT 1112
ID   ADM43217 standard; protein; 697 AA.
DE   Human methionine synthase reductase del Leu 576 variant.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; Score 71.5; DB 7; Length 697;
     Best Local Similarity   22.8%; Pred. No. 1e+02;
RESULT 1113
ID   AAB07591 standard; protein; 698 AA.
DE   A human methionine synthase reductase polypeptide.
PN   WO200042196-A2.
PD   20-JUL-2000.
PA   (UYMC-) UNIV MCGILL.
     Query Match   6.0%; Score 71.5; DB 3; Length 698;
     Best Local Similarity   22.8%; Pred. No. 1e+02;
RESULT 1114
ID   ABG00883 standard; protein; 698 AA.
DE   Novel human diagnostic protein #874.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   6.0%; Score 71.5; DB 4; Length 698;
     Best Local Similarity   22.8%; Pred. No. 1e+02;
RESULT 1115
ID   ADM43211 standard; protein; 698 AA.
DE   Human methionine synthase reductase Met221Ile variant.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; Score 71.5; DB 7; Length 698;
     Best Local Similarity   22.8%; Pred. No. 1e+02;
RESULT 1116
ID   ADM43213 standard; protein; 698 AA.
DE   Human methionine synthase reductase Cys37Tyr variant.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
     Query Match

PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; Score 71.5; DB 7; Length 698;
     Best Local Similarity   22.8%; Pred. No. 1e+02;
RESULT 1117
ID   ADM43207 standard; protein; 698 AA.
DE   Human wild-type methionine synthase reductase.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; Score 71.5; DB 7; Length 698;
     Best Local Similarity   22.8%; Pred. No. 1e+02;
RESULT 1118
ID   ADQ39857 standard; protein; 698 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   6.0%; Score 71.5; DB 8; Length 698;
     Best Local Similarity   22.8%; Pred. No. 1e+02;
RESULT 1119
ID   ADQ39858 standard; protein; 725 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1521.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   6.0%; Score 71.5; DB 8; Length 725;
     Best Local Similarity   22.8%; Pred. No. 1.1e+02;
RESULT 1120
ID   ADU05586 standard; protein; 725 AA.
DE   Novel bronchial cancer-associated human protein SeqID812.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.
     Query Match   6.0%; Score 71.5; DB 8; Length 725;
     Best Local Similarity   22.8%; Pred. No. 1.1e+02;
RESULT 1121
ID   AAY51606 standard; protein; 890 AA.
DE   Human wm1 protein.
PN   DE19845277-C1.
PD   09-MAR-2000.
PA   (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
     Query Match   6.0%; Score 71.5; DB 3; Length 890;
     Best Local Similarity   23.8%; Pred. No. 1.5e+02;
RESULT 1122
ID   ABB78282 standard; protein; 890 AA.
DE   Amino acid sequence of human wolframin polypeptide.
PN   WO200263307-A2.
PD   15-AUG-2002.
PA   (PHAA) PHARMACIA & UPJOHN CO.
     Query Match   6.0%; Score 71.5; DB 5; Length 890;
     Best Local Similarity   23.8%; Pred. No. 1.5e+02;
RESULT 1123
ID   ADD46013 standard; protein; 890 AA.
DE   Human Protein O76024, SEQ ID NO 11685.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   6.0%; Score 71.5; DB 7; Length 890;
     Best Local Similarity   23.8%; Pred. No. 1.5e+02;
RESULT 1124
ID   ADP69127 standard; protein; 890 AA.
DE   Human MP53 protein sequence SEQ ID NO:97.
PN   WO2003083047-A2.
PD   09-OCT-2003.
PA   (EXEL-) EXELIXIS INC.
     Query Match   6.0%; Score 71.5; DB 7; Length 890;

RESULT 1125
Best Local Similarity   23.8%;   Pred. No. 1.5e+02;
ID   ADY70426 standard; protein; 890 AA.
DE   Human beta-amyloid precursor protein, wolframin.
PN   WO2005023858-A1.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match
Best Local Similarity   23.8%;   Score 71.5;   DB 9;   Length 890;

RESULT 1126
Best Local Similarity   23.8%;   Pred. No. 1.5e+02;
ID   ADY70680 standard; protein; 890 AA.
DE   Human nicastrin/Psen2-complex member, wolframin protein.
PN   WO2005023833-A2.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match
Best Local Similarity   23.8%;   Score 71.5;   DB 9;   Length 890;

RESULT 1127
Best Local Similarity   23.8%;   Pred. No. 1.5e+02;
ID   AD122689 standard; protein; 2245 AA.
DE   Human disease detection and treatment (MDDT) protein - SEQ ID 138.
PN   WO2003062379-A2.
PD   31-JUL-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 7;   Length 2245;

RESULT 1128
Best Local Similarity   22.4%;   Pred. No. 5.2e+02;
ID   AAB42192 standard; protein; 2405 AA.
DE   Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.
PN   WO2000058473-A2.
PD   05-OCT-2000.
PA   (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 3;   Length 2405;

RESULT 1129
Best Local Similarity   22.4%;   Pred. No. 5.8e+02;
ID   AAB11404 standard; peptide; 2560 AA.
DE   Human FLAMINGO 1 homologue, SEQ ID NO:1774.
PN   WO2000157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 4;   Length 2560;

RESULT 1130
Best Local Similarity   22.4%;   Pred. No. 6.3e+02;
ID   ABU11556 standard; protein; 2894 AA.
DE   Human MDDT polypeptide SEQ ID 503.
PN   WO2002079449-A2.
PD   10-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 6;   Length 2894;

RESULT 1131
Best Local Similarity   22.4%;   Pred. No. 7.5e+02;
ID   AAU07054 standard; protein; 2923 AA.
DE   Human Flamingo protein encoded by cDNA splice variant.
PN   WO2002061003-A1.
PD   23-AUG-2001.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 4;   Length 2923;

RESULT 1132
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   AAM50866 standard; protein; 2923 AA.
DE   Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
PN   WO2002008765-A2.
PD   31-JAN-2002.
PA   (GENO-) APPLIED GENOMICS INC.
PA   (STRD) UNIV STANFORD.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 5;   Length 2923;

RESULT 1133
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ABP82018 standard; protein; 2923 AA.
DE   Human GPCR CELSR2 protein SEQ ID NO:524.
PN   WO2002061087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 6;   Length 2923;

RESULT 1134
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ADC15499 standard; protein; 2923 AA.
DE   Human GPCR protein EGF LAG seven-pass G-type receptor 2.
PN   US2003086934-A1.
PD   08-MAY-2003.
PA   (BOTS/) BOTSTEIN D.
PA   (BROW/) BROWN P O.
PA   (PERO/) PEROU C M.
PA   (RING/) RING B.
PA   (ROSS/) ROSS D.
PA   (SEIT/) SEITZ R.
PA   (VRIJ/) VAN DE RIJN J M.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 7;   Length 2923;

RESULT 1135
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ADC86479 standard; protein; 2923 AA.
DE   Human GPCR protein EGF LAG seven-pass G-type receptor 2.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 7;   Length 2923;

RESULT 1136
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ADE54407 standard; protein; 2923 AA.
DE   Human Protein XP_042739, SEQ ID NO 210.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 7;   Length 2923;

RESULT 1137
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ADE54411 standard; protein; 2923 AA.
DE   Human Protein XP_042739, SEQ ID NO 214.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 7;   Length 2923;

RESULT 1138
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ADO29245 standard; protein; 2923 AA.
DE   Human GPCR CELSR2, SEQ ID NO:346.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM/) PRIMAL INC.
Query Match
Best Local Similarity   6.0%;   Score 71.5;   DB 8;   Length 2923;

RESULT 1139
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ADY70314 standard; protein; 2923 AA.
DE   Human BACE1/PTK7-complex member, CELSR2 protein.
PN   WO2005023858-A1.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 9;   Length 2923;

RESULT 1140
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ADY70652 standard; protein; 2923 AA.
DE   Human BACE1, cadherin EGF LAG seven-pass G-type receptor 2.
PN   WO2005023833-A2.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match
Best Local Similarity   22.4%;   Score 71.5;   DB 9;   Length 2923;

RESULT 1141
Best Local Similarity   22.4%;   Pred. No. 7.6e+02;
ID   ADY70648 standard; protein; 2923 AA.
DE   Human BACE1-complex, cadherin seven-pass G-type receptor 2 protein.
PN   WO2005023833-A2.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match

RESULT 1142
Best Local Similarity 22.4%; Pred. No. 7.6e+02;
ID AAU74826 standard; protein; 2936 AA.
DE Human REPTR 9 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.4%; Score 71.5; DB 5; Length 2936;

RESULT 1143
Best Local Similarity 23.7%; Pred. No. 7.6e+02;
ID AAU07053 standard; protein; 2956 AA.
DE Human Flamingo polypeptide.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 22.4%; Score 71.5; DB 4; Length 2956;

RESULT 1144
Best Local Similarity 23.7%; Pred. No. 7.7e+02;
ID ADX40788 standard; protein; 3010 AA.
DE HCV Polymerase protein #11.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match 6.0%; Score 71.5; DB 9; Length 3010;

RESULT 1145
Best Local Similarity 23.7%; Pred. No. 7.9e+02;
ID AAR34468 standard; protein; 3011 AA.
DE Encoded by full-length Hepatitis C virus clone JK1-B.
PN JP05068562-A.
PD 23-MAR-1993.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
Query Match 6.0%; Score 71.5; DB 2; Length 3011;

RESULT 1146
Best Local Similarity 23.7%; Pred. No. 7.9e+02;
ID AAR31621 standard; protein; 3011 AA.
DE Hepatitis C virus (HCV) polyprotein.
PN WO9305365-A2.
PD 07-JAN-1993.
PA (CHIR) CHIRON CORP.
Query Match 6.0%; Score 71.5; DB 2; Length 3011;

RESULT 1147
Best Local Similarity 22.8%; Pred. No. 7.9e+02;
ID ABB67866 standard; protein; 5303 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30390.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 71.5; DB 4; Length 5303;

RESULT 1148
Best Local Similarity 29.5%; Pred. No. 1.7e+03;
ID ABB06793 standard; protein; 198 AA.
DE Human transmembrane 4 protein 22 SEQ ID NO:2.
PN CN1327990-A.
PD 26-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 29.5%; Score 71; DB 5; Length 198;

RESULT 1149
Best Local Similarity 24.5%; Pred. No. 21;
ID ADU08919 standard; protein; 223 AA.
DE Coronavirus membrane protein seqid 42.
PN WO2004096842-A2.
PD 11-NOV-2004.
PA (BCCA-) BC CANCER AGENCY.
Query Match 22.4%; Score 71; DB 8; Length 223;

RESULT 1150
Best Local Similarity 18.6%; Pred. No. 27;
ID ABR58398 standard; protein; 240 AA.
DE Human NOV17a.
PN WO200329423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 6; Length 240;

RESULT 1151
Best Local Similarity 24.9%; Pred. No. 36;
ID ABP26255 standard; protein; 295 AA.
DE Streptococcus polypeptide SEQ ID NO 1686.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 24.9%; Score 71; DB 5; Length 295;

RESULT 1152
Best Local Similarity 18.7%; Pred. No. 38;
ID ADX65958 standard; protein; 309 AA.
DE Plant full length insert polypeptide seqid 36801.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 18.7%; Score 71; DB 8; Length 309;

RESULT 1153
Best Local Similarity 19.7%; Pred. No. 39;
ID AAG72952 standard; protein; 310 AA.
DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 310;

RESULT 1154
Best Local Similarity 22.9%; Pred. No. 39;
ID AAR48717 standard; protein; 312 AA.
DE G-protein coupled human interleukin-8 receptor protein.
PN WO9405695-A1.
PD 17-MAR-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 5.9%; Score 71; DB 2; Length 312;

RESULT 1155
Best Local Similarity 19.7%; Pred. No. 39;
ID AAW02689 standard; peptide; 312 AA.
DE G-protein coupled human interleukin-8 receptor.
PN US5508384-A.
PD 16-APR-1996.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 5.9%; Score 71; DB 2; Length 312;

RESULT 1156
Best Local Similarity 22.9%; Pred. No. 39;
ID AAG72169 standard; protein; 312 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1850.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 312;

RESULT 1157
Best Local Similarity 22.9%; Pred. No. 39;
ID AAG72377 standard; protein; 312 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2058.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 312;

RESULT 1158
Best Local Similarity 22.9%; Pred. No. 39;
ID ADY08080 standard; protein; 364 AA.
DE Plant full length insert polypeptide seqid 63895.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
Query Match 5.9%; Score 71; DB 4; Length 312;

PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
RESULT 1159
Query Match
Best Local Similarity   18.7%;   Score 71;   DB 8;   Length 364;
ID   ABB54394 standard; protein; 391 AA.
DE   Lactococcus lactis protein ykiI.
PN   WO200177335-A2.
PD   18-OCT-2001.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
RESULT 1160
Best Local Similarity   20.3%;   Score 71;   DB 5;   Length 391;
Query Match
ID   ABB48413 standard; protein; 423 AA.
DE   Listeria monocytogenes protein #1117.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
RESULT 1161
Best Local Similarity   28.4%;   Score 71;   DB 5;   Length 423;
Query Match
ID   ADL05302 standard; protein; 423 AA.
DE   M. catarrhalis protein #1068.
PN   US6673910-B1.
PD   06-JAN-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
RESULT 1162
Best Local Similarity   38.0%;   Score 71;   DB 8;   Length 423;
Query Match
ID   ADJ95142 standard; protein; 444 AA.
DE   Novel NOVX protein sequence #185.
PN   WO2003040325-A2.
PD   15-MAY-2003.
PA   (CURA-) CURAGEN CORP.
RESULT 1163
Best Local Similarity   21.0%;   Score 71;   DB 7;   Length 444;
Query Match
ID   ADJ95144 standard; protein; 444 AA.
DE   Novel NOVX protein sequence #186.
PN   WO2003040325-A2.
PD   15-MAY-2003.
PA   (CURA-) CURAGEN CORP.
RESULT 1164
Best Local Similarity   21.0%;   Score 71;   DB 7;   Length 444;
Query Match
ID   ADU73808 standard; protein; 448 AA.
DE   Drosophila melanogaster Cbl-b.
PN   WO2004099388-A2.
PD   18-NOV-2004.
PA   (PROT-) PROTEOLOGICS INC.
RESULT 1165
Best Local Similarity   23.5%;   Score 71;   DB 8;   Length 448;
Query Match
ID   ADU69155 standard; protein; 448 AA.
DE   Fruit fly CBL-B protein.
PN   WO200408492-A2.
PD   18-NOV-2004.
PA   (PROT-) PROTEOLOGICS INC.
RESULT 1166
Best Local Similarity   23.5%;   Score 71;   DB 8;   Length 448;
Query Match
ID   ADW87442 standard; protein; 448 AA.
DE   Drosophila melanogaster CBL-B.
PN   WO2005007141-A2.
PD   27-JAN-2005.
PA   (PROT-) PROTEOLOGICS INC.
RESULT 1167
Best Local Similarity   23.5%;   Score 71;   DB 9;   Length 448;
Query Match
ID   ADP29417 standard; protein; 455 AA.
DE   Human secreted protein SEQ ID #184.
PN   WO200405732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
RESULT 1168
Best Local Similarity   24.3%;   Score 71;   DB 8;   Length 455;
Query Match
ID   ABU19912 standard; protein; 457 AA.
DE   Protein encoded by Prokaryotic essential gene #5439.
PN   WO200271183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 1169
Best Local Similarity   22.0%;   Score 71;   DB 6;   Length 457;
Query Match
ID   ADI24575 standard; protein; 470 AA.
DE   Human endogenous 5HT2A serotonin receptor.
PN   US2003224442-A1.
PD   04-DEC-2003.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
PA   (LIAW/) LIAW C W.
PA   (RUSS/) RUSSO J F.
PA   (THOM/) THOMSEN W J.
RESULT 1170
Best Local Similarity   23.7%;   Score 71;   DB 8;   Length 470;
Query Match
ID   AAR37659 standard; protein; 471 AA.
DE   Sequence encoded by cDNA.
PN   WO9311257-A2.
PD   10-JUN-1993.
PA   (BOEH) BOEHRINGER INGELHEIM INT GMBH.
RESULT 1171
Best Local Similarity   23.7%;   Score 71;   DB 2;   Length 471;
Query Match
ID   AAW23781 standard; protein; 471 AA.
DE   Human serotonin 5-HT2 receptor protein.
PN   US5661024-A.
PD   26-AUG-1997.
PA   (SYNA-) SYNAPTIC PHARM CORP.
RESULT 1172
Best Local Similarity   23.7%;   Score 71;   DB 2;   Length 471;
Query Match
ID   AAW77107 standard; protein; 471 AA.
DE   Human 5-HT2A serotonin receptor.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.
RESULT 1173
Best Local Similarity   23.7%;   Score 71;   DB 2;   Length 471;
Query Match
ID   AAY90640 standard; protein; 471 AA.
DE   Human mutant G protein-coupled receptor 5HT-2A.
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
RESULT 1174
Best Local Similarity   23.7%;   Score 71;   DB 3;   Length 471;
Query Match
ID   AAY90675 standard; protein; 471 AA.
DE   Human G protein-coupled receptor 5HT-2A (serotonin receptor).
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
RESULT 1175
Best Local Similarity   23.7%;   Score 71;   DB 3;   Length 471;
Query Match
ID   ABB07978 standard; protein; 471 AA.
DE   Human mutant 5-HT2 receptor sequence.
PN   US6383762-B1.
PD   07-MAY-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.
Query Match

Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1176
ID   ABP81765 standard; protein; 471 AA.
DE   Human 5-HT2A receptor protein SEQ ID NO:12.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match   5.9%; Score 71; DB 6; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1177
ID   ADC22641 standard; protein; 471 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #32.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
Query Match   5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1178
ID   ADC22747 standard; protein; 471 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #72.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
Query Match   5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1179
ID   ADE65844 standard; protein; 471 AA.
DE   Human serotonin 2A receptor.
PN   US2003170723-A1.
PD   11-SEP-2003.
PA   (SATO/) SATO T.
Query Match   5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1180
ID   ADH14220 standard; protein; 471 AA.
DE   Mutated human serotonin 5HT_2A.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
Query Match   5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1181
ID   ADH14114 standard; protein; 471 AA.
DE   Human serotonin 5HT_2A.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
Query Match   5.9%; Score 71; DB 7; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1182
ID   ADL50125 standard; protein; 471 AA.
DE   Human serotonin receptor 5HT2a.
PN   US2003167476-A1.
PD   04-SEP-2003.
PA   (CONK/) CONKLIN B R.
Query Match   5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1183
ID   ADO29506 standard; protein; 471 AA.
DE   Human GPCR HTR2A, SEQ ID NO:608.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
Query Match   5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1184
ID   ADQ39800 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1463.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1185
ID   ADQ39799 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1462.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1186
ID   ADQ39798 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1461.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1187
ID   ADU48367 standard; protein; 471 AA.
DE   Human serotonin 2A receptor protein.
PN   US2004229287-A1.
PD   18-NOV-2004.
PA   (AREN-) ARENA PHARM INC.
Query Match   5.9%; Score 71; DB 8; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1188
ID   ADX02782 standard; protein; 471 AA.
DE   Human 5-HT 2a receptor protein SeqID22.
PN   WO2005012254-A1.
PD   10-FEB-2005.
PA   (UYCO) UNIV COLUMBIA NEW YORK.
Query Match   5.9%; Score 71; DB 9; Length 471;
Best Local Similarity 23.7%; Pred. No. 69;

RESULT 1189
ID   AAY01626 standard; protein; 478 AA.
DE   Amino acid sequence of the human 5-HT2 receptor.
PN   US5885785-A.
PD   23-MAR-1999.
PA   (SYNA-) SYNAPTIC PHARM CORP.
Query Match   5.9%; Score 71; DB 2; Length 478;
Best Local Similarity 23.7%; Pred. No. 70;

RESULT 1190
ID   ABG70577 standard; protein; 480 AA.
DE   Human serotonin (5-HT2) receptor.
PN   US2002098548-A1.
PD   25-JUL-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.
Query Match   5.9%; Score 71; DB 5; Length 480;
Best Local Similarity 23.7%; Pred. No. 71;

RESULT 1191
ID   ABM70440 standard; protein; 493 AA.
DE   Photorhabdus luminescens protein sequence #3537.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
Query Match   5.9%; Score 71; DB 6; Length 493;
Best Local Similarity 23.5%; Pred. No. 73;

RESULT 1192
ID   ADE56383 standard; protein; 545 AA.
DE   Rat Protein 070536, SEQ ID NO 2235.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match   5.9%; Score 71; DB 7; Length 545;
Best Local Similarity 22.0%; Pred. No. 84;

RESULT 1193
ID   ADD48660 standard; protein; 545 AA.
DE   Rat Protein BAA25372, SEQ ID NO 14366.

PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   5.9%;
     Best Local Similarity   22.0%;
     Score 71; DB 7; Pred. No. 84; Length 545;

RESULT 1194
ID   ADS43584 standard; protein; 546 AA.
DE   Bacterial polypeptide #22014.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   5.9%;
     Best Local Similarity   26.2%;
     Score 71; DB 8; Pred. No. 85; Length 546;

RESULT 1195
ID   ABU26399 standard; protein; 559 AA.
DE   Aspergillus fumigatus essential gene protein #1057.
PN   WO200286090-A2.
PD   31-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.9%;
     Best Local Similarity   23.1%;
     Score 71; DB 6; Pred. No. 87; Length 559;

RESULT 1196
ID   ABP35686 standard; protein; 563 AA.
DE   Fungal ZBC protein sequence #112.
PN   WO200224865-A2.
PD   28-MAR-2002.
PA   (MICR-) MICROBIA INC.
     Query Match   5.9%;
     Best Local Similarity   19.1%;
     Score 71; DB 5; Pred. No. 88; Length 563;

RESULT 1197
ID   AAB20578 standard; protein; 564 AA.
DE   Mouse OCTN3 protein SEQ ID NO:1.
PN   WO200046368-A1.
PD   10-AUG-2000.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
     Query Match   5.9%;
     Best Local Similarity   21.4%;
     Score 71; DB 3; Pred. No. 88; Length 564;

RESULT 1198
ID   AEB36506 standard; protein; 603 AA.
DE   L. pneumophila protein SEQ ID NO 838.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   5.9%;
     Best Local Similarity   18.3%;
     Score 71; DB 9; Pred. No. 97; Length 603;

RESULT 1199
ID   ADQ96374 standard; protein; 631 AA.
DE   T cell activation associated protein #276.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match   5.9%;
     Best Local Similarity   21.3%;
     Score 71; DB 8; Pred. No. 1e+02; Length 631;

RESULT 1200
ID   ADQ96376 standard; protein; 631 AA.
DE   T cell activation associated protein #277.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match   5.9%;
     Best Local Similarity   21.3%;
     Score 71; DB 8; Pred. No. 1e+02; Length 631;

RESULT 1201
ID   ABB91532 standard; protein; 676 AA.
DE   Herbicidally active polypeptide SEQ ID NO 743.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB) BAYER AG.
     Query Match   5.9%;
     Best Local Similarity   22.3%;
     Score 71; DB 5; Pred. No. 1.1e+02; Length 676;

RESULT 1202
ID   AAE21800 standard; protein; 727 AA.
DE   Human HIPHUM 0000029 protein.
PN   GB2365432-A.
PD   20-FEB-2002.
PA   (GLAX) GLAXO GROUP LTD.
     Query Match   5.9%;
     Best Local Similarity   24.3%;
     Score 71; DB 6; Pred. No. 1.3e+02; Length 727;

RESULT 1203
ID   ABU54636 standard; protein; 727 AA.
DE   Human NOVX polypeptide #95.
PN   WO200281498-A2.
PD   17-OCT-2002.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.9%;
     Best Local Similarity   24.3%;
     Score 71; DB 5; Pred. No. 1.3e+02; Length 727;

RESULT 1204
ID   ADH76500 standard; protein; 727 AA.
DE   727 amino acid human neurotransmitter transporter protein.
PN   US2003219774-A1.
PD   27-NOV-2003.
PA   (SHAR/) SHARMA R.
PA   (RAMA/) RAMANATHAN C S.
PA   (WEST/) WESTPHAL R.
PA   (FEDE/) FEDER J N.
PA   (LEEL/) LEE L M.
     Query Match   5.9%;
     Best Local Similarity   24.3%;
     Score 71; DB 7; Pred. No. 1.3e+02; Length 727;

RESULT 1205
ID   ABR62929 standard; protein; 744 AA.
DE   Human neurotransmitter transporter.
PN   WO2003059947-A1.
PD   24-JUL-2003.
PA   (FARB) BAYER AG.
     Query Match   5.9%;
     Best Local Similarity   17.7%;
     Score 71; DB 4; Pred. No. 1.4e+02; Length 744;

RESULT 1206
ID   ABB60052 standard; protein; 792 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 6948.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.9%;
     Best Local Similarity   24.3%;
     Score 71; DB 7; Pred. No. 1.3e+02; Length 792;

RESULT 1207
ID   ABM90462 standard; protein; 929 AA.
DE   Rice abiotic stress responsive polypeptide SEQ ID NO:9184.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
     Query Match   5.9%;
     Best Local Similarity   20.6%;
     Score 71; DB 7; Pred. No. 1.8e+02; Length 929;

RESULT 1208
ID   AAR30616 standard; protein; 3010 AA.
DE   Polypeptide coded by Korean HCV full cDNA sequence LBC1.
PN   EP521318-A2.
PD   07-JAN-1993.
PA   (LUCK-) LUCKY LTD.
     Query Match   5.9%;
     Best Local Similarity   26.9%;
     Score 71; DB 2; Pred. No. 9e+02; Length 3010;

RESULT 1209
ID   AAR53417 standard; protein; 3010 AA.
DE   Blood transmissible NANBHV protein.
PN   JP06105690-A.
PD   19-APR-1994.
PA   (KAEN/) KAENO K.
     Query Match   5.9%;
     Best Local Similarity   26.9%;
     Score 71; DB 2; Pred. No. 9e+02; Length 3010;

RESULT 1210

ID ADX40817 standard; protein; 3010 AA.
DE HCV polymerase protein #40.
PN WO200501250502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match
Best Local Similarity 26.9%; Score 71; DB 9; Length 3010;

RESULT 1212
ID ADX40812 standard; protein; 3010 AA.
DE HCV polymerase protein #35.
PN WO200501250502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match
Best Local Similarity 26.9%; Score 71; Pred. No. 9e+02; DB 9; Length 3010;

RESULT 1211
ID ADX40783 standard; protein; 3010 AA.
DE HCV polymerase protein #6.
PN WO200501250502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match
Best Local Similarity 26.9%; Score 71; Pred. No. 9e+02; DB 9; Length 3010;

RESULT 1213
ID ABR8573 standard; protein; 3010 AA.
DE Bcrc amino acid sequence SEQ ID NO:40.
PN WO2003057708-A2.
PD 17-JUL-2003.
PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.
Query Match
Best Local Similarity 26.5%; Score 71; Pred. No. 9e+02; DB 9; Length 3010;

RESULT 1214
ID AAU01287 standard; protein; 218 AA.
DE Brassica napus fatty acid desaturase, Fad3C, partial sequence.
PN WO200125453-A2.
PD 12-APR-2001.
PA (MIAC-) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match
Best Local Similarity 29.3%; Score 70.5; Pred. No. 24; DB 4; Length 218;

RESULT 1215
ID AAU97208 standard; protein; 228 AA.
DE Portion of a wheat sugar transport protein encoded by wreln.pk0006.b4.
PN US6383776-B1.
PD 07-MAY-2002.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 21.6%; Score 70.5; Pred. No. 27; DB 5; Length 228;

RESULT 1216
ID ABU08333 standard; protein; 228 AA.
DE Wheat sugar transport protein #3.
PN US20021784468-A1.
PD 28-NOV-2002.
PA (ALLE-) ALLEN S M.
PA (HITZ-) HITZ W D.
PA (KINN-) KINNEY A J.
PA (TING-) TINGEY S V.
Query Match
Best Local Similarity 21.6%; Score 70.5; Pred. No. 29; DB 5; Length 228;

RESULT 1217
ID ADG47920 standard; protein; 228 AA.
DE Wheat Arabidopsis-like sugar transport protein #3.
PN US20021992917-A1.
PD 26-DEC-2002.
PA (HELE-) HELENTJARIS T G.
Query Match
Best Local Similarity 21.6%; Score 70.5; Pred. No. 29; DB 8; Length 228;

RESULT 1218
ID ABU17430 standard; protein; 275 AA.
DE Protein encoded by Prokaryotic essential gene #2957.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 21.6%; Score 70.5; DB 6; Length 275;

Best Local Similarity 22.8%; Pred. No. 37;

RESULT 1219
ID ADY06253 standard; protein; 283 AA.
DE Plant full length insert polypeptide seqid 62068.
PN US20040348888-A1.
PD 19-FEB-2004.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
PA (LIU/-) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 27.4%; Score 70.5; Pred. No. 39; DB 5; Length 283;

RESULT 1220
ID ABB55033 standard; protein; 285 AA.
DE Lactococcus lactis protein malG.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 26.1%; Score 70.5; Pred. No. 40; DB 5; Length 285;

RESULT 1221
ID ABB05467 standard; protein; 291 AA.
DE Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.
PN JP2001321171-A.
PD 20-NOV-2001.
PA (WARI/) WARISHI H.
PA (KUBI-) KUBOTA CORP.
Query Match
Best Local Similarity 29.4%; Score 70.5; Pred. No. 42; DB 5; Length 291;

RESULT 1222
ID ADA35787 standard; protein; 297 AA.
DE Acinetobacter baumannii protein #2948.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 24.1%; Score 70.5; Pred. No. 46; DB 6; Length 297;

RESULT 1223
ID ABM70358 standard; protein; 321 AA.
DE Photorhabdus luminescens protein sequence #3455.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (CNRS-) CNRS CENT NAT RECH SCI.
PA (INSP-) INST PASTEUR.
Query Match
Best Local Similarity 19.2%; Score 70.5; Pred. No. 48; DB 6; Length 321;

RESULT 1224
ID ADH22355 standard; protein; 330 AA.
DE Human receptor & membrane associated protein (REMAP) SeqID5.
PN WO2003104395-A2.
PD 18-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 24.2%; Score 70.5; DB 8; Length 330;

RESULT 1225
ID ADK68232 standard; protein; 343 AA.
DE Novel NOVX protein #79.
PN WO200308485124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 30.0%; Score 70.5; Pred. No. 51; DB 7; Length 343;

RESULT 1226
ID ADH72226 standard; protein; 343 AA.
DE Human protein of the invention NOV5a SEQ ID NO:1122.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 30.0%; Score 70.5; DB 8; Length 343;

RESULT 1227

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ID   ADR49221 standard; protein; 343 AA.
DE   Human NOV10a protein.
PN   US20040162236-A1.
PD   19-AUG-2004.
PA   (ALSO/) ALSOBROOK J.
PA   (BENT/) BENTO P.
PA   (BOLD/) BOLDOG F.
PA   (BURG/) BURGESS C.
PA   (CASM/) CASMAN S.
PA   (BOKO/) BOKOR J C.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (FERN/) FERNANDES E.
PA   (GERL/) GERLACH V.
PA   (GROS/) GROSSE W.
PA   (GUNT/) GUNTHER E.
PA   (GUSE/) GUSEV V.
PA   (HEYE/) HEYES M.
PA   (LEPL/) LEPLEY D.
PA   (LILL/) LI L.
PA   (MACD/) MACDOUGALL J R.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLET I.
PA   (PATT/) PATTURAJAN M.
PA   (PEYM/) PEYMAN J A.
PA   (RAST/) RASTELLI L.
PA   (RIEG/) RIEGER D.
PA   (SHEN/) SHENOY S.
PA   (SHIM/) SHIMKETS R.
PA   (SMIT/) SMITHSON G.
PA   (STON/) STONE D.
PA   (VERN/) VERNET C.
PA   (VOSS/) VOSS E.
     Query Match
     Best Local Similarity    5.9%;    Score 30.0%;  Pred. No. 51;  DB 8;  Length 343;

RESULT 1228
ID   ADY15182 standard; protein; 350 AA.
DE   PRO polypeptide SEQ ID NO 988.
PN   WO200501696962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   18.5%;    Score 70.5;   Pred. No. 52;  DB 9;  Length 350;

RESULT 1229
ID   ADY15180 standard; protein; 350 AA.
DE   PRO polypeptide SEQ ID NO 986.
PN   WO200501696962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   18.5%;    Score 70.5;   Pred. No. 52;  DB 9;  Length 350;

RESULT 1230
ID   ADR40543 standard; protein; 363 AA.
DE   Ovine melatonin receptor O46608 protein.
PN   US20041161823-A1.
PD   19-AUG-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
     Query Match
     Best Local Similarity   18.5%;    Score 70.5;   Pred. No. 52;  DB 8;  Length 363;

RESULT 1231
ID   AAR69518 standard; protein; 365 AA.
DE   Prostaglandin-EP3-9 receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI ) MERCK FROSST CANADA INC.
     Query Match
     Best Local Similarity   23.1%;    Score 70.5;   Pred. No. 55;  DB 2;  Length 365;

RESULT 1232
ID   AAE38521 standard; protein; 365 AA.
DE   Human PTGER3 protein isoform, EP3b.
PN   WO200306447I-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match
     Best Local Similarity   24.2%;    Score 70.5;   Pred. No. 55;  DB 7;  Length 365;

RESULT 1233
ID   ADI35077 standard; protein; 365 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.
PN   US20032244393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match
     Best Local Similarity   24.2%;    Score 70.5;   Pred. No. 55;  DB 8;  Length 365;

RESULT 1234
ID   ADI15889 standard; protein; 365 AA.
DE   Human prostaglandin EP3 receptor #3.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR ) ALLERGAN INC.
PA   (UYAR-) UNIV ARIZONA.
     Query Match
     Best Local Similarity   24.2%;    Score 70.5;   Pred. No. 55;  DB 8;  Length 365;

RESULT 1235
ID   ADR67864 standard; protein; 365 AA.
DE   Prostaglandin E2 EP3 III.
PN   WO200407483O-A2.
PD   02-SEP-2004.
PA   (FARB ) BAYER HEALTHCARE AG.
     Query Match
     Best Local Similarity   24.2%;    Score 70.5;   Pred. No. 55;  DB 8;  Length 365;

RESULT 1236
ID   ADS21429 standard; protein; 366 AA.
DE   Bacterial polypeptide #10462.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match
     Best Local Similarity   21.2%;    Score 70.5;   Pred. No. 56;  DB 8;  Length 366;

RESULT 1237
ID   ADF04358 standard; protein; 367 AA.
DE   Bacterial polypeptide #471.
PN   US605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match
     Best Local Similarity   33.3%;    Score 70.5;   Pred. No. 56;  DB 7;  Length 367;

RESULT 1238
ID   AAE38520 standard; protein; 374 AA.
DE   Human PTGER3 protein isoform, EP3d.
PN   WO200306447I-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match
     Best Local Similarity   24.2%;    Score 70.5;   Pred. No. 57;  DB 7;  Length 374;

RESULT 1239
ID   ADI35075 standard; protein; 374 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.
PN   US20032244393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match
     Best Local Similarity   24.2%;    Score 70.5;   Pred. No. 57;  DB 8;  Length 374;

RESULT 1240
ID   AAR48711 standard; protein; 379 AA.
DE   G-protein coupled rat serotonin 2 receptor protein.
PN   WO9405695-A1.
PD   17-MAR-1994.
PA   (UYNY ) UNIV NEW YORK STATE.
     Query Match
     Best Local Similarity    5.9%;    Score 70.5;                  DB 2;  Length 379;
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Best Local Similarity   22.9%;   Pred. No. 58;

RESULT 1241
ID   AAW02683 standard; peptide; 379 AA.
DE   G-protein coupled rat serotonin 2 receptor.
PN   US5508384-A.
PD   16-APR-1996.
PA   (UYNY) UNIV NEW YORK STATE.
Query Match   22.9%;   Score 70.5;   DB 2;   Length 379;
Best Local Similarity

RESULT 1242
ID   AAR69517 standard; protein; 388 AA.
DE   Prostaglandin-EP3-21 receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI) MERCK FROSST CANADA INC.
Query Match   24.2%;   Score 70.5;   DB 2;   Length 388;
Best Local Similarity   5.9%;   Pred. No. 60;

RESULT 1243
ID   AAE38513 standard; protein; 388 AA.
DE   Human PTGER3 protein isoform, EP3c.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match   5.9%;   Score 70.5;   DB 7;   Length 388;
Best Local Similarity   24.2%;   Pred. No. 60;

RESULT 1244
ID   ADI35061 standard; protein; 388 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (ALLR) ALLERGAN INC.
Query Match   24.2%;   Score 70.5;   DB 8;   Length 388;
Best Local Similarity   5.9%;   Pred. No. 60;

RESULT 1245
ID   AD115887 standard; protein; 388 AA.
DE   Human prostaglandin EP3 receptor #2.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR) ALLERGAN INC.
Query Match   24.2%;   Score 70.5;   DB 8;   Length 388;
Best Local Similarity   5.9%;   Pred. No. 60;

RESULT 1246
ID   ADS13753 standard; protein; 388 AA.
DE   Human prostaglandin E2 EP3 II polypeptide.
PN   WO2004075813-A2.
PD   10-SEP-2004.
PA   (FARB) BAYER HEALTHCARE AG.
Query Match   24.2%;   Score 70.5;   DB 8;   Length 388;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1247
ID   AAR69516 standard; protein; 390 AA.
DE   Prostaglandin-EP3-alpha receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI) MERCK FROSST CANADA INC.
Query Match   24.2%;   Score 70.5;   DB 2;   Length 390;
Best Local Similarity   5.9%;   Pred. No. 61;

RESULT 1248
ID   AAE38516 standard; protein; 390 AA.
DE   Human PTGER3 protein isoform, EP3a1.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match   5.9%;   Score 70.5;   DB 7;   Length 390;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1249
ID   AAE38517 standard; protein; 390 AA.
DE   Human PTGER3 protein isoform, EP3a2.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match   5.9%;   Score 70.5;   DB 7;   Length 390;
Best Local Similarity

Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1250
ID   AD135067 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (ALLR) ALLERGAN INC.
Query Match   5.9%;   Score 70.5;   DB 8;   Length 390;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1251
ID   AD135069 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (ALLR) ALLERGAN INC.
Query Match   5.9%;   Score 70.5;   DB 8;   Length 390;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1252
ID   AD135898 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 receptor #4.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR) ALLERGAN INC.
Query Match   5.9%;   Score 70.5;   DB 8;   Length 390;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1253
ID   AD115885 standard; protein; 390 AA.
DE   Human prostaglandin EP3 receptor #1.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR) ALLERGAN INC.
Query Match   5.9%;   Score 70.5;   DB 8;   Length 390;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1254
ID   ADR70434 standard; protein; 390 AA.
DE   Human prostaglandin E2 EP3 protein.
PN   WO2004075814-A2.
PD   10-SEP-2004.
PA   (FARB) BAYER HEALTHCARE AG.
Query Match   5.9%;   Score 70.5;   DB 8;   Length 390;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1255
ID   ADS76168 standard; protein; 390 AA.
DE   Prostaglandin E2 EP3 I.
PN   WO2004075814-A2.
PD   10-SEP-2004.
PA   (FARB) BAYER HEALTHCARE AG.
Query Match   5.9%;   Score 70.5;   DB 8;   Length 390;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1256
ID   AAW57411 standard; protein; 393 AA.
DE   Human prostaglandin EP3-VI receptor.
PN   JP10113185-A.
PD   06-MAY-1998.
PA   (ONOY) ONO PHARM CO LTD.
Query Match   5.9%;   Score 70.5;   DB 2;   Length 393;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1257
ID   AAE38519 standard; protein; 393 AA.
DE   Human PTGER3 protein isoform, EP3e.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match   5.9%;   Score 70.5;   DB 7;   Length 393;
Best Local Similarity   24.2%;   Pred. No. 61;

RESULT 1258
ID   AAE38523 standard; protein; 393 AA.
DE   Human PTGER3 protein isoform, EP3-VI.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.

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                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 7;   Length 393;
ID   AD135081 standard; protein; 393 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1260
                    Query Match
                    Best Local Similarity   5.9%;   Score 70.5;   DB 8;   Length 393;
ID   AD135073 standard; protein; 393 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1261
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 8;   Length 393;
ID   AAW57410 standard; protein; 393 AA.
DE   Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN   JP10113185-A.
PD   06-MAY-1998.
PA   (ONOY ) ONO PHARM CO LTD.

RESULT 1262
                    Query Match
                    Best Local Similarity   5.9%;   Score 70.5;   DB 2;   Length 402;
ID   ABP81904 standard; protein; 402 AA.
DE   Human EP3-V receptor.
PN   WO2000261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.

RESULT 1263
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 6;   Length 402;
ID   AAE38522 standard; protein; 402 AA.
DE   Human PTGER3 protein isoform, EP3-V.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1264
                    Query Match
                    Best Local Similarity   5.9%;   Score 70.5;   DB 7;   Length 402;
ID   AD135079 standard; protein; 402 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1265
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 8;   Length 402;
ID   AD055167 standard; protein; 402 AA.
DE   Protein #69 with increased gene expression in renal cell carcinoma.
PN   WO200040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.

RESULT 1266
                    Query Match
                    Best Local Similarity   5.9%;   Score 70.5;   DB 8;   Length 402;
ID   AD029620 standard; protein; 402 AA.
DE   Human GPCR PTGER3, SEQ ID NO:722.
PN   WO2004032842-A2.
PD   22-APR-2004.
PA   (VAND-) VAN ANDEL INST.

RESULT 1267
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 9;   Length 402;
ID   AD209834 standard; protein; 402 AA.
DE   Human breast cancer marker DKFZp586M0723 protein.
PN   EP1522594-A2.
PD   13-APR-2005.
PA   (FARB ) BAYER HEALTHCARE AG.
                    Query Match
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                    Best Local Similarity   24.2%;   Pred. No. 63;
RESULT 1268
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 7;   Length 407;
ID   AAE38514 standard; protein; 407 AA.
DE   Human PTGER3 protein isoform, EP3g.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1269
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 8;   Length 407;
ID   AD135063 standard; protein; 407 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1270
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 8;   Length 425;
ID   AAE38518 standard; protein; 425 AA.
DE   Human PTGER3 protein isoform, EP3f.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1271
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 7;   Length 425;
ID   AD135071 standard; protein; 425 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1272
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 8;   Length 433;
ID   AAE38515 standard; protein; 433 AA.
DE   Human PTGER3 protein isoform, EP3h.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1273
                    Query Match
                    Best Local Similarity   24.2%;   Score 70.5;   DB 7;   Length 433;
ID   AD135065 standard; protein; 433 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.

RESULT 1274
                    Query Match
                    Best Local Similarity   5.9%;   Score 70.5;   DB 2;   Length 480;
ID   AAW98431 standard; protein; 480 AA.
DE   H. Pylori GHPO 446 protein.
PN   WO9843478-A1.
PD   08-OCT-1998.
PA   (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 1275
                    Query Match
                    Best Local Similarity   23.1%;   Score 70.5;   DB 2;   Length 494;
ID   ADY09805 standard; protein; 494 AA.
DE   Plant full length insert polypeptide seqid 65620.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (PRIM-) PRIMAL INC.
PA   (LIU/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.

RESULT 1276
                    Query Match
                    Best Local Similarity   21.4%;   Score 70.5;   DB 8;   Length 499;
ID   ABP40525 standard; protein; 499 AA.
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DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.

RESULT 1277
Query Match   5.9%;   Score 70.5;   DB 5;   Length 499;
Best Local Similarity 20.5%;   Pred. No. 85;
ID ADS06092 standard; protein; 499 AA.
DE Staphylococcus epidermidis polypeptide seqid 5387.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

RESULT 1278
Query Match   5.9%;   Score 70.5;   DB 6;   Length 521;
Best Local Similarity 23.7%;   Pred. No. 91;
ID ABU30473 standard; protein; 521 AA.
DE Protein encoded by Prokaryotic essential gene #16000.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

RESULT 1279
Query Match   5.9%;   Score 70.5;   DB 5;   Length 539;
Best Local Similarity 26.0%;   Pred. No. 95;
ID AAU97213 standard; protein; 539 AA.
DE Wheat sugar transport protein encoded by wlk8.pk0001.a11.
PN US6383776-B1.
PD 07-MAY-2002.
PA (DUPO/) DU PONT DE NEMOURS & CO E I.
PA (ALLE/) ALLEN S M.
PA (HITZ/) HITZ W D.
PA (KINN/) KINNEY A J.
PA (TING/) TINGEY S V.
PA (HELE/) HELENTJARIS T G.

RESULT 1280
Query Match   5.9%;   Score 70.5;   DB 6;   Length 539;
Best Local Similarity 26.0%;   Pred. No. 95;
ID ABU08338 standard; protein; 539 AA.
DE Wheat sugar transport protein #4.
PN US2002178468-A1.
PD 28-NOV-2002.
PA (DUPO/) DU PONT DE NEMOURS & CO E I.

RESULT 1281
Query Match   5.9%;   Score 70.5;   DB 8;   Length 539;
Best Local Similarity 26.0%;   Pred. No. 95;
ID ADG47930 standard; protein; 539 AA.
DE Wheat Beta-vulgaris-like sugar transport protein #1.
PN US20020199217-A1.
PD 26-DEC-2002.
PA (HELE/) HELENTJARIS T G.

RESULT 1282
Query Match   5.9%;   Score 70.5;   DB 6;   Length 548;
Best Local Similarity 26.0%;   Pred. No. 95;
ID ABU27418 standard; protein; 548 AA.
DE Protein encoded by Prokaryotic essential gene #12945.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

RESULT 1283
Query Match   5.9%;   Score 70.5;   DB 8;   Length 556;
Best Local Similarity 24.0%;   Pred. No. 97;
ID ADN22789 standard; protein; 556 AA.
DE Bacterial polypeptide #5442.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

RESULT 1284
Query Match   5.9%;   Score 70.5;   DB 8;   Length 599;
Best Local Similarity 21.1%;   Pred. No. 99;
ID ADD46023 standard; protein; 599 AA.
DE Rat Protein P23378, SEQ ID NO 11695.
PN WO20030016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

RESULT 1285
Query Match   5.9%;   Score 70.5;   DB 7;   Length 599;
Best Local Similarity 20.1%;   Pred. No. 1.1e+02;
ID ABW02687 standard; protein; 599 AA.
DE Rattus norvegicus neuronal GABA transporter (GAT-1).
PN US2003143729-A1.
PD 31-JUL-2003.
PA (SYNA-) SYNAPTIC PHARM CORP.

RESULT 1286
Query Match   5.9%;   Score 70.5;   DB 7;   Length 600;
Best Local Similarity 20.1%;   Pred. No. 1.1e+02;
ID AAM78767 standard; protein; 600 AA.
DE Human protein SEQ ID NO 1429.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

RESULT 1287
Query Match   5.9%;   Score 70.5;   DB 4;   Length 662;
Best Local Similarity 19.5%;   Pred. No. 1.1e+02;
ID ADJ64315 standard; protein; 662 AA.
DE Cartilage differentiation inhibiting protein, SEQ ID 10.
PN WO2004013326-A1.
PD 12-FEB-2004.
PA (FARB) BAYER AG.

RESULT 1288
Query Match   5.9%;   Score 70.5;   DB 5;   Length 700;
Best Local Similarity 22.7%;   Pred. No. 1.3e+02;
ID ABB92892 standard; protein; 700 AA.
DE Herbicidally active polypeptide SEQ ID NO 10.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.

RESULT 1289
Query Match   5.9%;   Score 70.5;   DB 8;   Length 717;
Best Local Similarity 25.8%;   Pred. No. 1.4e+02;
ID AAB56721 standard; protein; 717 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO:1299.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.

RESULT 1290
Query Match   5.9%;   Score 70.5;   DB 5;   Length 740;
Best Local Similarity 22.4%;   Pred. No. 1.4e+02;
ID ADG47941 standard; protein; 740 AA.
DE Arabidopsis thaliana-like sugar transport protein #2.
PN US20020199217-A1.
PD 26-DEC-2002.
PA (HELE/) HELENTJARIS T G.

RESULT 1291
Query Match   5.9%;   Score 70.5;   DB 3;   Length 766;
Best Local Similarity 22.8%;   Pred. No. 1.5e+02;
ID AAG39555 standard; protein; 766 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
PN EP1033405-A2.
PD 06-SEP-2000.

RESULT 1292
Query Match   5.9%;   Score 70.5;   DB 3;   Length 815;
Best Local Similarity 21.3%;   Pred. No. 1.5e+02;
ID AAG39554 standard; protein; 815 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
PN EP1033405-A2.
PD 06-SEP-2000.

RESULT 1293
Query Match   5.9%;   Score 70.5;   DB 3;   Length 927;
Best Local Similarity 21.3%;   Pred. No. 1.7e+02;
ID AAG39553 standard; protein; 927 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
PN EP1033405-A2.

PD   06-SEP-2000.
Query Match   5.9%;   Score 70.5;   DB 3;   Length 927;
Best Local Similarity   21.3%;   Pred. No. 2e+02;
RESULT 1294
ID   ABP73754 standard; protein; 1026 AA.
DE   Candida albicans essential protein SEQ ID NO 7591.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   5.9%;   Score 70.5;   DB 5;   Length 1026;
Best Local Similarity   22.3%;   Pred. No. 2.3e+02;
RESULT 1295
ID   AAW17057 standard; protein; 1027 AA.
DE   Candida albicans chitin synthase (CHS1).
PN   WO9716540-A1.
PD   09-MAY-1997.
PA   (CHEM-) CHEMGENICS PHARM INC.
Query Match   5.9%;   Score 70.5;   DB 2;   Length 1027;
Best Local Similarity   22.3%;   Pred. No. 2.3e+02;
RESULT 1296
ID   ADH22510 standard; protein; 1147 AA.
DE   Human transporter & ion channel (TRICH) protein SeqID8.
PN   WO200309444-A2.
PD   13-NOV-2003.
PA   (INCY-) INCYTE CORP.
Query Match   5.9%;   Score 70.5;   DB 8;   Length 1147;
Best Local Similarity   19.5%;   Pred. No. 2.7e+02;
RESULT 1297
ID   ADK18350 standard; protein; 1163 AA.
DE   Human NOVX protein #2.
PN   WO200305785-A2.
PD   17-JUL-2003.
PA   (CURA-) CURAGEN CORP.
Query Match   5.9%;   Score 70.5;   DB 7;   Length 1163;
Best Local Similarity   19.5%;   Pred. No. 2.8e+02;
RESULT 1298
ID   ADM29274 standard; protein; 1163 AA.
DE   Human novel protein NOV2b.
PN   WO200306628-A2.
PD   07-AUG-2003.
PA   (CURA-) CURAGEN CORP.
Query Match   5.9%;   Score 70.5;   DB 7;   Length 1163;
Best Local Similarity   19.5%;   Pred. No. 2.8e+02;
RESULT 1299
ID   AAW53863 standard; peptide; 1780 AA.
DE   Human gravin polypeptide.
PN   US5741890-A.
PD   21-APR-1998.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
Query Match   5.9%;   Score 70.5;   DB 2;   Length 1780;
Best Local Similarity   34.8%;   Pred. No. 5e+02;
RESULT 1300
ID   AAB15380 standard; protein; 1780 AA.
DE   Human gravin protein sequence.
PN   US6090929-A.
PD   18-JUL-2000.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
Query Match   5.9%;   Score 70.5;   DB 3;   Length 1780;
Best Local Similarity   34.8%;   Pred. No. 5e+02;
RESULT 1301
ID   AAO17365 standard; protein; 1781 AA.
DE   Human gravin.
PN   EP1191107-A2.
PD   27-MAR-2002.
PA   (SCHD) SCHERING AG.
Query Match   5.9%;   Score 70.5;   DB 5;   Length 1781;
Best Local Similarity   34.8%;   Pred. No. 5e+02;
RESULT 1302
ID   ABU03477 standard; protein; 1781 AA.
DE   Angiogenesis-associated human protein sequence #22.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match   5.9%;   Score 70.5;   DB 6;   Length 1781;
Best Local Similarity   34.8%;   Pred. No. 5e+02;
RESULT 1303
ID   ABB97448 standard; protein; 1783 AA.
DE   Novel human protein SEQ ID NO: 716.
PN   WO200222660-A2.
PD   21-MAR-2002.
PA   (HYSB-) HYSEQ INC.
Query Match   5.9%;   Score 70.5;   DB 5;   Length 1783;
Best Local Similarity   34.8%;   Pred. No. 5e+02;
RESULT 1304
ID   ABG21018 standard; protein; 1795 AA.
DE   Novel human diagnostic protein #21009.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSB-) HYSEQ INC.
Query Match   5.9%;   Score 70.5;   DB 4;   Length 1795;
Best Local Similarity   34.8%;   Pred. No. 5e+02;
RESULT 1305
ID   AAG34242 standard; protein; 185 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match   5.9%;   Score 70.5;   DB 3;   Length 185;
Best Local Similarity   26.2%;   Pred. No. 25;
RESULT 1306
ID   AAG34241 standard; protein; 189 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41630.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match   5.9%;   Score 70;   DB 3;   Length 189;
Best Local Similarity   26.2%;   Pred. No. 25;
RESULT 1307
ID   AAW44944 standard; protein; 225 AA.
DE   Avian infectious bronchitis virus glycoprotein M.
PN   FR2751225-A1.
PD   23-JAN-1998.
PA   (INM) RHONE MERIEUX SA.
Query Match   5.9%;   Score 70;   DB 2;   Length 225;
Best Local Similarity   21.6%;   Pred. No. 32;
RESULT 1308
ID   ADB09893 standard; protein; 226 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:3730.
PN   WO200304304-A2.
PD   12-JUN-2003.
PA   (AMH) WYETH HOLDINGS CORP.
Query Match   5.9%;   Score 70;   DB 6;   Length 226;
Best Local Similarity   24.1%;   Pred. No. 33;
RESULT 1309
ID   ABB69790 standard; protein; 235 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 36162.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   5.9%;   Score 70;   DB 3;   Length 235;
Best Local Similarity   26.2%;   Pred. No. 34;
RESULT 1310
ID   ADS96502 standard; protein; 256 AA.
DE   Drosophila melanogaster protein, SEQ ID 123.
PN   WO200439999-A2.
PD   13-MAY-2004.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match   5.9%;   Score 70;   DB 4;   Length 256;
Best Local Similarity   20.2%;   Pred. No. 39;
RESULT 1311
ID   ADT05703 standard; protein; 256 AA.

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DE   Haemophilus influenzae (NTHi) protein - SEQ ID 739.
PN   WO020407894 9-A2
PD   16-SEP-2004.
PA   (CHIL-) CHILDRENS HOSPITAL INC.
     Query Match       5.9%;   Score 70;   DB 8;   Length 256;
     Best Local Similarity  18.3%;   Pred. No. 39;

RESULT 1313
ID   AAG53762 standard; protein; 274 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68478.
PN   EP1033405-A2.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match       5.9%;   Score 70;   DB 3;   Length 274;
     Best Local Similarity  26.0%;   Pred. No. 43;

RESULT 1314
ID   AAG53761 standard; protein; 287 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68477.
PN   EP1033405-A2.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match       5.9%;   Score 70;   DB 3;   Length 287;
     Best Local Similarity  26.0%;   Pred. No. 45;

RESULT 1315
ID   ABU35677 standard; protein; 292 AA.
DE   Protein encoded by Prokaryotic essential gene #21204.
PN   WO020277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match       5.9%;   Score 70;   DB 8;   Length 292;
     Best Local Similarity  22.5%;   Pred. No. 47;

RESULT 1316
ID   ADK48488 standard; protein; 307 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 5003.
PN   US6699703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match       5.9%;   Score 70;   DB 6;   Length 307;
     Best Local Similarity  26.2%;   Pred. No. 50;

RESULT 1317
ID   AAR72985 standard; protein; 333 AA.
DE   Epsilon opioid receptor.
PN   WO9512670-A1.
PD   11-MAY-1995.
PA   (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.
     Query Match       5.9%;   Score 70;   DB 2;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1318
ID   AAY90613 standard; protein; 333 AA.
DE   Human G protein-coupled receptor GPR8.
PN   WO020022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
     Query Match       5.9%;   Score 70;   DB 3;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1319
ID   AAY90647 standard; protein; 333 AA.
DE   Human mutant G protein-coupled receptor GPR8 (T259X).
PN   WO020022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
     Query Match       5.9%;   Score 70;   DB 3;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1320
ID   AAU01297 standard; protein; 333 AA.
DE   Human G-protein receptor 8, GPR 8, mutant N127A.
PN   WO020127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K. M.
     Query Match       5.9%;   Score 70;   DB 4;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1321
ID   AAU01295 standard; protein; 333 AA.
DE   Human G-protein receptor 8, GPR 8.
PN   WO020127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K. M.
     Query Match       5.9%;   Score 70;   DB 4;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1322
ID   AAU01298 standard; protein; 333 AA.
DE   Human G-protein receptor 8, GPR 8, mutant T259E.
PN   WO020127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K. M.
     Query Match       5.9%;   Score 70;   DB 4;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1323
ID   ABB84683 standard; protein; 333 AA.
DE   Human GPR8-ligand related protein #1.
PN   WO020198494-A1.
PD   27-DEC-2001.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match       5.9%;   Score 70;   DB 5;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1324
ID   ABB84723 standard; protein; 333 AA.
DE   Human GPR8-ligand related protein #3.
PN   WO020198494-A1.
PD   27-DEC-2001.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match       5.9%;   Score 70;   DB 5;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1325
ID   ABG65918 standard; protein; 333 AA.
DE   G protein-coupled receptor related peptide #6.
PN   WO020244368-A1.
PD   06-JUN-2002.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match       5.9%;   Score 70;   DB 5;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1326
ID   ABU61448 standard; protein; 333 AA.
DE   Screening method related protein #1.
PN   WO020293161-A1.
PD   21-NOV-2002.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match       5.9%;   Score 70;   DB 6;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1327
ID   ABJ37874 standard; protein; 333 AA.
DE   GPR7 ligand related human protein SEQ ID No 84.
PN   WO020102847-A1.
PD   27-DEC-2002.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match       5.9%;   Score 70;   DB 6;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1328
ID   ABP81897 standard; protein; 333 AA.
DE   Human G protein-coupled receptor GPR8 protein SEQ ID NO:279.
PN   WO020261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match       5.9%;   Score 70;   DB 6;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1329
ID   ABR57245 standard; protein; 333 AA.
DE   Human GPR8 protein SEQ ID NO:84.
PN   WO020345994-A1.
PD   05-JUN-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match       5.9%;   Score 70;   DB 7;   Length 333;
     Best Local Similarity  23.6%;   Pred. No. 56;

RESULT 1330
ID   ADC22691 standard; protein; 333 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #44.
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PN   US655339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1331
ID   ADC22535 standard; protein; 333 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #5.
PN   US655339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1332
ID   ADC51793 standard; protein; 333 AA.
DE   Human GPR8, SEQ ID 4.
PN   WO200305236-A1.
PD   17-JUL-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1333
ID   ABR61545 standard; protein; 333 AA.
DE   Human GPR8 receptor polypeptide.
PN   WO200308123-A2.
PD   02-OCT-2003.
PA   (FARB) BAYER AG.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1334
ID   ADG41976 standard; protein; 333 AA.
DE   Human GPR8 polypeptide.
PN   JP200309867-A.
PD   14-JAN-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1335
ID   ADH14008 standard; protein; 333 AA.
DE   Human GPR8.
PN   US200310529-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1336
ID   ADH14164 standard; protein; 333 AA.
DE   Mutated human GPR8.
PN   US200310529-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1337
ID   ADG12852 standard; protein; 333 AA.
DE   Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
PN   WO200309779-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
     Query Match   5.9%; Score 70; DB 8; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1338
ID   ADO29700 standard; protein; 333 AA.
DE   Human GPCR GPR8, SEQ ID NO:802.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Best Local Similarity   23.6%; Score 70; DB 8; Length 333;
     Query Match   5.9%; Pred. No. 56;

RESULT 1339
ID   ADO31044 standard; protein; 333 AA.
DE   Human GPR8 protein SEQ ID NO:73.
PN   WO200404130-A1.
PD   21-MAY-2004.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.9%; Score 70; DB 8; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1340
ID   ADQ19919 standard; protein; 333 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.
PN   WO200404938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match   5.9%; Score 70; DB 8; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1341
ID   ADS14162 standard; protein; 333 AA.
DE   Human GPR8 ligand protein SeqID 73.
PN   WO200408485-A1.
PD   23-SEP-2004.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.9%; Score 70; DB 8; Length 333;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1342
ID   ADV24041 standard; protein; 333 AA.
DE   Neuropeptide W antibody associated polypeptide seqid 17.
PN   WO200416382-A1.
PD   09-DEC-2004.
PA   (TAKE) TAKEDA PHARM CO LTD.
     Query Match   5.9%; Score 70; DB 9; Length 333;
     Best Local Similarity   23.6%; Pred. No. 59;

RESULT 1343
ID   ADG12854 standard; protein; 347 AA.
DE   Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
PN   WO200309779-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
     Query Match   5.9%; Score 70; DB 8; Length 347;
     Best Local Similarity   23.6%; Pred. No. 56;

RESULT 1344
ID   ABG30839 standard; protein; 364 AA.
DE   Human calcium channel protein.
PN   WO200252003-A2.
PD   04-JUL-2002.
PA   (FARB) BAYER AG.
     Query Match   5.9%; Score 70; DB 5; Length 364;
     Best Local Similarity   25.0%; Pred. No. 63;

RESULT 1345
ID   ADG12856 standard; protein; 364 AA.
DE   Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
PN   WO200309779-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
     Query Match   5.9%; Score 70; DB 8; Length 364;
     Best Local Similarity   23.6%; Pred. No. 63;

RESULT 1346
ID   ADO28778 standard; protein; 364 AA.
DE   Human GPR8-enhanced receptor.
PN   US200409194-A1.
PD   13-MAY-2004.
PA   (OAKL/) OAKLEY R H.
PA   (BARA/) BARAK L S.
PA   (LAPO/) LAPORTE S A.
PA   (CARO/) CARON M G.
     Query Match   5.9%; Score 70; DB 8; Length 364;
     Best Local Similarity   23.6%; Pred. No. 63;

RESULT 1347
ID   ADX44597 standard; protein; 364 AA.
DE   Enhanced human G-protein coupled receptor 8 - SEQ ID 56.
PN   WO200501287-A2.
PD   10-FEB-2005.
PA   (NORA-) NORAK BIOSCIENCES INC.
     Best Local Similarity   23.6%; Score 70; DB 8; Length 364;
     Query Match   5.9%; Pred. No. 63;

RESULT 1348
Query Match   5.9%; Score 70; DB 9; Length 364;
Best Local Similarity   23.6%; Pred. No. 63;
ID   ADY83827 standard; protein; 364 AA.
DE   hGPR8-enhanced receptor.
PN   WO200529035-A2.
PD   31-MAR-2005.
PA   (NORA-) NORAK BIOSCIENCES INC.

RESULT 1349
Query Match   5.9%; Score 70; DB 9; Length 364;
Best Local Similarity   23.6%; Pred. No. 63;
ID   ADG12858 standard; protein; 378 AA.
DE   HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.
PN   WO2003097795-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.

RESULT 1350
Query Match   5.9%; Score 70; DB 8; Length 378;
Best Local Similarity   23.6%; Pred. No. 67;
ID   ADN49121 standard; protein; 388 AA.
DE   Mouse oxytocin receptor protein.
PN   US200408688l-A1.
PD   06-MAY-2004.
PA   (RAMA/) RAMANATHAN C S.
PA   (GOPA/) GOPAL S.
PA   (MINT/) MINTIER G A.
PA   (FEDE/) FEDER J.

RESULT 1351
Query Match   5.9%; Score 70; DB 8; Length 388;
Best Local Similarity   24.8%; Pred. No. 69;
ID   ADC29591 standard; protein; 388 AA.
DE   Human protein, SEQ ID NO:693.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.

RESULT 1352
Query Match   5.9%; Score 70; DB 8; Length 388;
Best Local Similarity   24.8%; Pred. No. 69;
ID   ADA54410 standard; protein; 388 AA.
DE   Mouse GPCR OXTR, SEQ ID 1978.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.

RESULT 1353
Query Match   5.9%; Score 70; DB 6; Length 399;
Best Local Similarity   22.9%; Pred. No. 72;
ID   ABG99947 standard; protein; 399 AA.
DE   Human novel polypeptide #60.
PN   WO200274961-A1.
PD   26-SEP-2002.
PA   (HYSE-) HYSEQ INC.

RESULT 1354
Query Match   5.9%; Score 70; DB 7; Length 425;
Best Local Similarity   22.9%; Pred. No. 78;
ID   ADC96947 standard; protein; 425 AA.
DE   E. faecium protein sequence SEQ ID 6574.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.

RESULT 1355
Query Match   5.9%; Score 70; DB 6; Length 470;
Best Local Similarity   25.9%; Pred. No. 90;
ID   ADA34110 standard; protein; 470 AA.
DE   Acinetobacter baumannii protein #1271.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.

RESULT 1356
Query Match   5.9%; Score 70; DB 6; Length 470;
Best Local Similarity   23.5%; Pred. No. 90;
ID   ABM67264 standard; protein; 474 AA.
DE   Photorhabdus luminescens protein sequence #361.

PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.

RESULT 1357
Query Match   5.9%; Score 70; DB 6; Length 474;
Best Local Similarity   22.9%; Pred. No. 91;
ID   AAE16787 standard; protein; 475 AA.
DE   Human transporter and ion channel-24 (TRICH-24) protein.
PN   WO200192304-A2.
PD   06-DEC-2001.
PA   (INCY-) INCYTE GENOMICS INC.

RESULT 1358
Query Match   5.9%; Score 70; DB 5; Length 475;
Best Local Similarity   25.0%; Pred. No. 91;
ID   ADA89683 standard; protein; 506 AA.
DE   Staphylococcus aureus antigenic protein #222.
PN   WO2003011899-A2.
PD   13-FEB-2003.
PA   (UYSH-) UNIV SHEFFIELD.

RESULT 1359
Query Match   5.9%; Score 70; DB 6; Length 506;
Best Local Similarity   20.1%; Pred. No. 1e+02;
ID   ABM72414 standard; protein; 506 AA.
DE   Staphylococcus aureus protein #1654.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (BIOS-) BIOSYNEXUS INC.

RESULT 1360
Query Match   5.9%; Score 70; DB 6; Length 506;
Best Local Similarity   20.1%; Pred. No. 1e+02;
ID   AAE21176 standard; protein; 540 AA.
DE   Human TRICH-20 protein.
PN   WO200212340-A2.
PD   14-FEB-2002.
PA   (INCY-) INCYTE GENOMICS INC.

RESULT 1361
Query Match   5.9%; Score 70; DB 5; Length 540;
Best Local Similarity   25.0%; Pred. No. 1.1e+02;
ID   AAM39017 standard; protein; 552 AA.
DE   Human polypeptide SEQ ID NO 2162.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.

RESULT 1362
Query Match   5.9%; Score 70; DB 4; Length 552;
Best Local Similarity   25.0%; Pred. No. 1.1e+02;
ID   ABU18262 standard; protein; 602 AA.
DE   Protein encoded by Prokaryotic essential gene #3789.
PN   WO200227183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.

RESULT 1363
Query Match   5.9%; Score 70; DB 6; Length 602;
Best Local Similarity   25.0%; Pred. No. 1.3e+02;
ID   ABU33453 standard; protein; 637 AA.
DE   Protein encoded by Prokaryotic essential gene #18980.
PN   WO200227183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.

RESULT 1364
Query Match   5.9%; Score 70; DB 6; Length 637;
Best Local Similarity   23.1%; Pred. No. 1.4e+02;
ID   AEB39900 standard; protein; 637 AA.
DE   L. pneumophila protein SEQ ID NO 4232.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
Query Match   5.9%; Score 70; DB 9; Length 637;

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Best Local Similarity   22.3%;   Pred. No. 1.4e+02;

RESULT 1365
ID    AAY91335 standard; protein; 640 AA.
DE    Group B Streptococcus protein sequence SEQ ID NO:68.
PN    WO20006736-A2.
PD    10-FEB-2000.
PA    (MICR-) MICROBIAL TECHNICS LTD.
      Query Match             21.4%;   Score 70;   DB 3;   Length 640;
      Best Local Similarity    5.9%;   Pred. No. 1.4e+02;

RESULT 1366
ID    AEB36499 standard; protein; 647 AA.
DE    L. pneumophila protein SEQ ID NO 831.
PN    WO2005049642-A2.
PD    02-JUN-2005.
PA    (INSP ) INST PASTEUR.
PA    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA    (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match             22.3%;   Score 70;   DB 9;   Length 647;
      Best Local Similarity    5.9%;   Pred. No. 1.4e+02;

RESULT 1367
ID    ABM83818 standard; protein; 695 AA.
DE    Human diagnostic and therapeutic pprotein SEQ ID NO:4067.
PN    WO2004023973-A2.
PD    25-MAR-2004.
PA    (INCY-) INCYTE CORP.
      Query Match             28.6%;   Score 70;   DB 8;   Length 695;
      Best Local Similarity    5.9%;   Pred. No. 1.5e+02;

RESULT 1368
ID    ADL04660 standard; protein; 767 AA.
DE    M. catarrhalis protein #426.
PN    US6673910-B1.
PD    06-JAN-2004.
PA    (SHIM/) SHIMOTOYA K.
      Query Match             24.6%;   Score 70;   DB 2;   Length 767;
      Best Local Similarity    5.9%;   Pred. No. 1.8e+02;

RESULT 1369
ID    AAR53921 standard; protein; 1041 AA.
DE    HCV fusion protein corresp. to N-terminal of ORF.
PN    JP06092996-A.
PD    05-APR-1994.
PA    (GENO-) GENOME THERAPEUTICS CORP.
      Query Match             21.3%;   Score 70;   DB 8;   Length 1041;
      Best Local Similarity    5.9%;   Pred. No. 2.5e+02;

RESULT 1370
ID    ADS24062 standard; protein; 1049 AA.
DE    Bacterial polypeptide #13095.
PN    US2003233675-A1.
PD    18-DEC-2003.
PA    (HINK/) HINKLE G J.
PA    (CAOY/) CAO Y.
PA    (SLAT/) SLATER S C.
PA    (CHEN/) CHEN X.
PA    (GOLD/) GOLDMAN B S.
      Query Match             23.4%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1371
ID    ADU69762 standard; protein; 1049 AA.
DE    S agalactiae hyperimmune serum reactive antigen seqid 457.
PN    WO200409242-A2.
PD    18-NOV-2004.
PA    (INTE-) INTERCELL AG.
      Query Match             18.8%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1372
ID    ADU69581 standard; protein; 1049 AA.
DE    S agalactiae hyperimmune serum reactive antigen seqid 276.
PN    WO200409242-A2.
PD    18-NOV-2004.
PA    (INTE-) INTERCELL AG.
      Query Match             18.8%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1373
ID    ADU69756 standard; protein; 1049 AA.
DE    S agalactiae hyperimmune serum reactive antigen seqid 451.
PN    WO200409242-A2.
PD    18-NOV-2004.
PA    (INTE-) INTERCELL AG.
      Query Match             18.8%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1374
ID    ADV87847 standard; protein; 1049 AA.
DE    Streptococcus agalactiae protein sequence, SEQ ID 241.
PN    FR2824074-A1.
PD    31-OCT-2002.
PA    (INSP ) INST PASTEUR.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match             18.8%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1375
ID    ADV79100 standard; protein; 1049 AA.
DE    Streptococcus agalactiae protein, SEQ ID 241.
PN    WO200292818-A2.
PD    21-NOV-2002.
PA    (INSP ) INST PASTEUR.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match             18.8%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1376
ID    ADV82666 standard; protein; 1049 AA.
DE    Streptococcus agalactiae protein, SEQ ID 3807.
PN    WO200292818-A2.
PD    21-NOV-2002.
PA    (INSP ) INST PASTEUR.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match             18.8%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1377
ID    ADV81299 standard; protein; 1049 AA.
DE    Streptococcus agalactiae protein, SEQ ID 2440.
PN    WO200292818-A2.
PD    21-NOV-2002.
PA    (INSP ) INST PASTEUR.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match             18.8%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1378
ID    ADV82607 standard; protein; 1049 AA.
DE    Streptococcus agalactiae protein, SEQ ID 3748.
PN    WO200292818-A2.
PD    21-NOV-2002.
PA    (INSP ) INST PASTEUR.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match             18.8%;   Score 70;   DB 8;   Length 1049;
      Best Local Similarity    5.9%;   Pred. No. 2.7e+02;

RESULT 1379
ID    ADP07803 standard; protein; 138 AA.
DE    Human secreted protein, seq id 286.
PN    WO200404200-A2.
PD    21-MAY-2004.
PA    (HUMA-) HUMAN GENOME SCI INC.
      Query Match             22.0%;   Score 69.5;   DB 8;   Length 138;
      Best Local Similarity    5.8%;   Pred. No. 2.7e+02;

RESULT 1380
ID    ADA3664 standard; protein; 198 AA.
DE    Acinetobacter baumannii protein #825.
PN    US6562958-B1.
PD    13-MAY-2003.
PA    (GENO-) GENOME THERAPEUTICS CORP.
      Query Match             23.3%;   Score 69.5;   DB 6;   Length 198;
      Best Local Similarity    5.8%;   Pred. No. 2.7e+02;

RESULT 1381
ID    ADB09276 standard; protein; 201 AA.
DE    Alloiococcus otitis antigenic protein SEQ ID NO:3216.
PN    WO2003048304-A2.
PD    12-JUN-2003.
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PA   (AMHP ) WYETH HOLDINGS CORP.
     Query Match
     Best Local Similarity  26.0%;  Score 69.5;  DB 6;  Length 201;  Pred. No. 32;

RESULT 1382
ID   AEB41646 standard; protein; 201 AA.
DE   L. pneumophila protein SEQ ID NO 5978.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP ) INST PASTEUR.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match
     Best Local Similarity  17.6%;  Score 69.5;  DB 9;  Length 201;  Pred. No. 34;

RESULT 1383
ID   AAU29449 standard; protein; 210 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #70.
PN   WO200168858-A2.
PD   20-SEP-2001.
PA   (PHAA ) PHARMACIA & UPJOHN CO.
PA   (VOGE/) VOGELI G.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 4;  Length 210;  Pred. No. 34;

RESULT 1384
ID   ABG60737 standard; protein; 218 AA.
DE   Novel G protein coupled receptor (nGCPR-x) #70.
PN   US2002058306-A1.
PD   16-MAY-2002.
PA   (PHAA ) PHARMACIA & UPJOHN CO.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 4;  Length 218;  Pred. No. 36;

RESULT 1385
ID   AAU01288 standard; protein; 210 AA.
DE   Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.
PN   WO200125453-A2.
PD   12-APR-2001.
PA   (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.
     Query Match
     Best Local Similarity  29.3%;  Score 69.5;  DB 4;  Length 210;  Pred. No. 42;

RESULT 1386
ID   ADB09278 standard; protein; 247 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO.3218.
PN   WO200304304-A2.
PD   23-MAY-2002.
PA   (AMHP ) WYETH HOLDINGS CORP.
     Query Match
     Best Local Similarity  26.0%;  Score 69.5;  DB 6;  Length 247;  Pred. No. 42;

RESULT 1387
ID   ABG66935 standard; protein; 253 AA.
DE   Novel G-protein coupled receptor related protein #12.
PN   WO200240539-A2.
PD   12-JUN-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match
     Best Local Similarity  24.2%;  Score 69.5;  DB 5;  Length 253;  Pred. No. 44;

RESULT 1388
ID   ABB62542 standard; protein; 261 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 14418.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match
     Best Local Similarity  27.7%;  Score 69.5;  DB 4;  Length 261;  Pred. No. 46;

RESULT 1389
ID   ABO80446 standard; protein; 270 AA.
DE   Pseudomonas aeruginosa polypeptide #12621.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match
     Best Local Similarity  22.1%;  Score 69.5;  DB 7;  Length 270;  Pred. No. 48;

RESULT 1390
ID   ADE86076 standard; protein; 296 AA.
DE   Streptomyces hygroscopicus ABC transporter.
PN   WO2003082909-A1.
PD   09-OCT-2003.
PA   (AMHP ) WYETH.
     Query Match
     Best Local Similarity  21.0%;  Score 69.5;  DB 7;  Length 296;  Pred. No. 54;

RESULT 1391
ID   AAG71524 standard; protein; 308 AA.
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1205.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (YEDA ) YEDA RES & DEV CO LTD.
PA   (DIGI-) DIGISCENTS.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 4;  Length 308;  Pred. No. 57;

RESULT 1392
ID   ABB44525 standard; protein; 308 AA.
DE   Human GPCR3 polypeptide SEQ ID NO 9.
PN   WO200174904-A2.
PD   11-OCT-2001.
PA   (CURA-) CURAGEN CORP.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 5;  Length 308;  Pred. No. 57;

RESULT 1393
ID   AAU24742 standard; protein; 308 AA.
DE   Human olfactory receptor AOLFR242.
PN   WO200168805-A2.
PD   20-SEP-2001.
PA   (SENO-) SENOMYX INC.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 4;  Length 308;  Pred. No. 57;

RESULT 1394
ID   ABP95703 standard; protein; 308 AA.
DE   Human GPCR polypeptide SEQ ID NO 216.
PN   WO200216548-A2.
PD   28-FEB-2002.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 5;  Length 308;  Pred. No. 57;

RESULT 1395
ID   AAU95729 standard; protein; 308 AA.
DE   Human olfactory and pheromone G protein-coupled receptor #216.
PN   WO200224726-A2.
PD   28-MAR-2002.
PA   (CHEM-) CHEMCOM SA.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 5;  Length 308;  Pred. No. 57;

RESULT 1396
ID   AAU85362 standard; protein; 308 AA.
DE   G-coupled olfactory receptor #223.
PN   WO200198526-A2.
PD   27-DEC-2001.
PA   (SENO-) SENOMYX INC.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 5;  Length 308;  Pred. No. 57;

RESULT 1397
ID   ADC86333 standard; protein; 308 AA.
DE   Human GPCR protein SEQ ID NO:786.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
     Query Match
     Best Local Similarity  20.9%;  Score 69.5;  DB 7;  Length 308;  Pred. No. 57;

RESULT 1398
ID   ABW02126 standard; protein; 308 AA.
DE   Human GPCR3 protein.
PN   US2003195335-A1.
PD   16-OCT-2003.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (CASM/) CASMAN S.
PA   (ALSO/) ALSOBROOK J P.
PA   (BURG/) BURGESS C E.
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PA (PADI/) PADIGARU M.
PA (TAYL/) TAYLOR S.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (STON/) STONE D J.
PA (SMIT/) SMITHSON G.
PA (MACD/) MACDOUGALL J R.
Query Match   5.8%;
Best Local Similarity 20.9%;   Score 69.5;   DB 7;   Length 308;

RESULT 1399
ID ABR01671 standard; protein; 316 AA.
DE Human G protein coupled receptor SEQ ID 202.
PN WO2003000735-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match   5.8%;
Best Local Similarity 20.9%;   Score 69.5;   DB 6;   Length 316;

RESULT 1400
ID ADU20551 standard; protein; 317 AA.
DE A. thaliana At5g67210 homologue.
PN WO2004092349-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match   5.8%;
Best Local Similarity 33.7%;   Score 69.5;   DB 8;   Length 317;

RESULT 1401
ID ADU20398 standard; protein; 317 AA.
DE A. thaliana drought tolerance-associated protein At5g67210.
PN WO2004092349-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match   5.8%;
Best Local Similarity 33.7%;   Score 69.5;   DB 8;   Length 317;

RESULT 1402
ID AAY35360 standard; protein; 321 AA.
DE Chlamydia pneumoniae involved in the virulence process.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match   5.8%;
Best Local Similarity 21.4%;   Score 69.5;   DB 2;   Length 321;

RESULT 1403
ID ADC33485 standard; protein; 321 AA.
DE Yeast ARV1.
PN US6566512-B1.
PD 20-MAY-2003.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match   5.8%;
Best Local Similarity 18.8%;   Score 69.5;   DB 7;   Length 321;

RESULT 1404
ID ADE37749 standard; protein; 321 AA.
DE Yeast ARV1 (ARE-2 Required for viability).
PN US2003186879-A1.
PD 02-OCT-2003.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match   5.8%;
Best Local Similarity 18.8%;   Score 69.5;   DB 7;   Length 321;

RESULT 1405
ID AAU53139 standard; protein; 327 AA.
DE Propionibacterium acnes immunogenic protein #14035.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match   5.8%;
Best Local Similarity 18.8%;   Score 69.5;   DB 4;   Length 327;

RESULT 1406
ID ABM49658 standard; protein; 327 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14334.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match   5.8%;
Best Local Similarity 25.5%;   Score 69.5;   DB 4;   Length 327;

RESULT 1407
ID ADH10684 standard; protein; 354 AA.
DE Rat Sprague-Dawley putative GCR polypeptide.
PN WO2003106484-A1.
PD 18-DEC-2003.
PA (META-) METABOLEX INC.
Query Match   5.8%;
Best Local Similarity 22.0%;   Score 69.5;   DB 8;   Length 354;

RESULT 1408
ID AAY05489 standard; protein; 382 AA.
DE Human EDG-2 protein sequence.
PN WO9919513-A2.
PD 22-APR-1999.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
Query Match   5.8%;
Best Local Similarity 20.2%;   Score 69.5;   DB 2;   Length 382;

RESULT 1409
ID AAU00302 standard; protein; 382 AA.
DE LPA receptor-related amino acid sequence #1.
PN WO200112838-A2.
PD 26-NOV-2002.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
Query Match   5.8%;
Best Local Similarity 20.2%;   Score 69.5;   DB 4;   Length 382;

RESULT 1410
ID ABG76099 standard; protein; 382 AA.
DE Human lysophosphatidic acid (LPA) receptor EDG-1.
PN US6485922-B1.
PD 18-OCT-2001.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
Query Match   5.8%;
Best Local Similarity 20.2%;   Score 69.5;   DB 6;   Length 382;

RESULT 1411
ID ABB47613 standard; protein; 400 AA.
DE Listeria monocytogenes protein #317.
PN WO200177335-A2.
PD 03-OCT-2002.
PA (INSP) INST PASTEUR.
Query Match   5.8%;
Best Local Similarity 22.9%;   Score 69.5;   DB 5;   Length 400;

RESULT 1412
ID ABU32698 standard; protein; 400 AA.
DE Protein encoded by Prokaryotic essential gene #18225.
PN WO200277183-A2.
PD 09-JAN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match   5.8%;
Best Local Similarity 22.9%;   Score 69.5;   DB 6;   Length 400;

RESULT 1413
ID ADL12060 standard; protein; 401 AA.
DE Drosophila dmTrp1 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match   5.8%;
Best Local Similarity 22.9%;   Score 69.5;   DB 7;   Length 401;

RESULT 1414
ID ABB60948 standard; protein; 415 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9636.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match   5.8%;
Best Local Similarity 20.9%;   Score 69.5;   DB 7;   Length 401;

RESULT 1415
ID ADL12059 standard; protein; 415 AA.
DE Drosophila dmTrpla12 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match   5.8%;
Best Local Similarity 20.9%;   Score 69.5;   DB 4;   Length 415;

PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match   5.8%; Score 69.5; DB 7; Length 415;
Best Local Similarity 20.9%; Pred. No. 87;

RESULT 1416
ID   AB866992 standard; protein; 428 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 27768.
PN   WO2001171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   5.8%; Score 69.5; DB 4; Length 428;
Best Local Similarity 20.9%; Pred. No. 91;

RESULT 1417
ID   ADI12058 standard; protein; 428 AA.
DE   Drosophila dmTrplalt1 protein.
PN   WO2003002137-A2.
PD   09-JAN-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match   5.8%; Score 69.5; DB 7; Length 428;
Best Local Similarity 20.9%; Pred. No. 91;

RESULT 1418
ID   AAY41284 standard; protein; 444 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
DE   CI-NT-his fusion protein encoded by plasmid pLJM6-09.
PN   WO9953033-A1.
PD   21-OCT-1999.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (UYVA-) UNIV VANDERBILT.
Query Match   5.8%; Score 69.5; DB 2; Length 444;
Best Local Similarity 23.6%; Pred. No. 95;

RESULT 1419
ID   AAG30875 standard; protein; 453 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match   5.8%; Score 69.5; DB 3; Length 453;
Best Local Similarity 23.3%; Pred. No. 98;

RESULT 1420
ID   ADK47327 standard; protein; 453 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 3842.
PN   US6699703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match   5.8%; Score 69.5; DB 8; Length 453;
Best Local Similarity 23.6%; Pred. No. 98;

RESULT 1421
ID   ADR95087 standard; protein; 461 AA.
DE   Novel S. pneumoniae protein sequence, SEQ ID 3722.
PN   US6800744-B1.
PD   05-OCT-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match   5.8%; Score 69.5; DB 8; Length 461;
Best Local Similarity 24.4%; Pred. No. 1e+02;

RESULT 1422
ID   AEA58957 standard; protein; 461 AA.
DE   Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:3722.
PN   US2005136404-A1.
PD   23-JUN-2005.
PA   (DOUC/) DOUCETTE-STAMM L A.
Query Match   5.8%; Score 69.5; DB 8; Length 461;
Best Local Similarity 24.4%; Pred. No. 1e+02;

RESULT 1423
ID   AAG30874 standard; protein; 476 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (BUSH/) BUSH D.
Query Match   5.8%; Score 69.5; DB 9; Length 476;
Best Local Similarity 24.4%; Pred. No. 1e+02;

RESULT 1424
ID   ADN22349 standard; protein; 477 AA.
DE   Bacterial polypeptide #5002.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match   5.8%; Score 69.5; DB 8; Length 477;
Best Local Similarity 21.2%; Pred. No. 1.1e+02;

RESULT 1425
ID   ADS28512 standard; protein; 490 AA.
DE   Bacterial polypeptide #17545.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match   5.8%; Score 69.5; DB 8; Length 490;
Best Local Similarity 23.5%; Pred. No. 1.1e+02;

RESULT 1426
ID   ABO61637 standard; protein; 494 AA.
DE   Klebsiella pneumoniae polypeptide seqid 8154.
PN   US6610836-B1.
PD   26-AUG-2003.
Query Match   5.8%; Score 69.5; DB 7; Length 494;
Best Local Similarity 22.0%; Pred. No. 1.1e+02;

RESULT 1427
ID   AAY41278 standard; protein; 500 AA.
DE   Fusion protein containing rabbit prostaglandin E2BP3 receptor.
PN   WO9953033-A1.
PD   21-OCT-1999.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (UYVA-) UNIV VANDERBILT.
Query Match   5.8%; Score 69.5; DB 2; Length 500;
Best Local Similarity 23.3%; Pred. No. 1.1e+02;

RESULT 1428
ID   AAG30873 standard; protein; 503 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36986.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match   5.8%; Score 69.5; DB 3; Length 503;
Best Local Similarity 23.6%; Pred. No. 1.2e+02;

RESULT 1429
ID   AAY92829 standard; protein; 535 AA.
DE   C. pneumoniae CPN100557 processed antigen.
PN   WO2002024765-A2.
PD   04-MAY-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
Query Match   5.8%; Score 69.5; DB 3; Length 535;
Best Local Similarity 21.4%; Pred. No. 1.2e+02;

RESULT 1430
ID   ADR13717 standard; protein; 540 AA.
DE   Amidase, SEQ ID 54.
PN   WO2004069848-A2.
PD   19-AUG-2004.
PA   (DIVE-) DIVERSA CORP.
Query Match   5.8%; Score 69.5; DB 8; Length 540;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;

RESULT 1431
ID   AAY92828 standard; protein; 547 AA.
DE   C. pneumoniae CPN100557 antigen.
PN   WO2002024765-A2.
PD   04-MAY-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
Query Match   5.8%; Score 69.5; DB 3; Length 547;
Best Local Similarity 23.7%; Pred. No. 1.3e+02;

RESULT 1432
ID   ABU26764 standard; protein; 547 AA.
DE   Protein encoded by Prokaryotic essential gene #12291.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   5.8%; Score 69.5; DB 6; Length 547;
Best Local Similarity 21.4%; Pred. No. 1.3e+02;

RESULT 1433

ID ABU31940 standard; protein; 551 AA.
DE Protein encoded by Prokaryotic essential gene #17467.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 23.6%; DB 6; Length 551;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1434
ID AAY01650 standard; protein; 557 AA.
DE A protein with cation transporting activity.
PN WO913072-A1.
PD 18-MAR-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 2; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1435
ID AAY83929 standard; protein; 557 AA.
DE Human carnitine transporter protein OCTN2.
PN WO20014210-A1.
PD 16-MAR-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 3; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1436
ID ABG03029 standard; protein; 557 AA.
DE Novel human diagnostic protein #3020.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 4; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1437
ID ABB82979 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 3242598.
PN WO20029053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1438
ID ABB82980 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 4507005.
PN WO20029053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1439
ID ABB07242 standard; protein; 557 AA.
DE Human p53 modifying protein, SEQ ID 202.
PN WO20029122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1440
ID ADE09321 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #387.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1441
ID ADE09261 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #327.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1442
ID ADE23817 standard; protein; 557 AA.

DE PRO polypeptide SEQ ID NO:995.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 5.8%; Score 69.5; DB 8; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1443
ID ADY79867 standard; protein; 557 AA.
DE Amino acid sequence of a human SLC22A5 polypeptide.
PN WO2005026724-A2.
PD 24-MAR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 5.8%; Score 69.5; DB 9; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.3e+02;

RESULT 1444
ID ADA34637 standard; protein; 559 AA.
DE Acinetobacter baumannii protein #1798.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 559;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;

RESULT 1445
ID ABO62908 standard; protein; 564 AA.
DE Klebsiella pneumoniae polypeptide seqid 9425.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 564;
Best Local Similarity 23.6%; Pred. No. 1.3e+02;

RESULT 1446
ID ABB89665 standard; protein; 568 AA.
DE Human polypeptide SEQ ID NO 2041.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 5; Length 568;
Best Local Similarity 22.4%; Pred. No. 1.3e+02;

RESULT 1447
ID ADB65515 standard; protein; 573 AA.
DE Human protein encoded by clone TESTI20271790.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 5.8%; Score 69.5; DB 7; Length 573;
Best Local Similarity 22.7%; Pred. No. 1.4e+02;

RESULT 1448
ID ABB47410 standard; protein; 579 AA.
DE Listeria monocytogenes protein #114.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 69.5; DB 5; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.4e+02;

RESULT 1449
ID ABU32703 standard; protein; 579 AA.
DE Protein encoded by Prokaryotic essential gene #18230.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.4e+02;

RESULT 1450
ID ABP65234 standard; protein; 599 AA.
DE Hypoxia-regulated protein #108.
PN WO20024665-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 5.8%; Score 69.5; DB 5; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.4e+02;

RESULT 1451
ID AAE38584 standard; protein; 599 AA.

DE   Human GAT1 GABA transporter protein.
PN   WO2003061573-A2.
PD   31-JUL-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity   19.6%; Score 69.5; DB 7; Length 599;
RESULT 1452
ID   ADD46025 standard; protein; 599 AA.
DE   Human Protein P30531, SEQ ID NO 11697.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
Query Match
Best Local Similarity   19.6%; Score 69.5; DB 7; Length 599;
RESULT 1453
ID   AAY41285 standard; protein; 656 AA.
DE   CI-77A-TL fusion protein encoded by plasmid pLJM5-42T.
PN   WO9953033-A1.
PD   21-OCT-1999.
PA   (UVVA-) UNIV VANDERBILT.
Query Match
Best Local Similarity   23.6%; Score 69.5; DB 2; Length 656;
RESULT 1454
ID   ABP40194 standard; protein; 660 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity   27.2%; Score 69.5; DB 5; Length 660;
RESULT 1455
ID   ADS07250 standard; protein; 660 AA.
DE   Staphylococcus epidermidis polypeptide seqid 6545.
PN   US2004147734-A1.
PD   29-JUL-2004.
PA   (DOUC/) DOUCETTE-STAMM L.
PA   (BUSH/) BUSH D.
Query Match
Best Local Similarity   27.2%; Score 69.5; DB 8; Length 660;
RESULT 1456
ID   AAV17390 standard; protein; 663 AA.
DE   Human vesicle membrane protein-like protein 3.
PN   WO9921994-A2.
PD   06-MAY-1999.
PA   (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity   22.0%; Score 69.5; DB 2; Length 663;
RESULT 1457
ID   ADM83092 standard; protein; 663 AA.
DE   Human vesicle membrane protein (VMP)2.
PN   US2003175787-A1.
PD   18-SEP-2003.
PA   (INCY-) INCYTE CORP.
Query Match
Best Local Similarity   22.0%; Score 69.5; DB 8; Length 663;
RESULT 1458
ID   ADJ64317 standard; protein; 663 AA.
DE   Cartilage differentiation inhibiting protein, SEQ ID 12.
PN   WO2004013326-A1.
PD   12-FEB-2004.
PA   (ASAH) ASAHI KASEI KK.
Query Match
Best Local Similarity   22.0%; Score 69.5; DB 8; Length 663;
RESULT 1459
ID   ADQ96536 standard; protein; 663 AA.
DE   T cell activation associated protein #357.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match
Best Local Similarity   22.0%; Score 69.5; DB 8; Length 663;
RESULT 1460

ID   ADY19824 standard; protein; 663 AA.
DE   PRO polypeptide SEQ ID NO 5630.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   22.0%; Score 69.5; DB 9; Length 663;
RESULT 1461
ID   ADY14394 standard; protein; 663 AA.
DE   PRO polypeptide SEQ ID NO 200.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   22.0%; Score 69.5; DB 9; Length 663;
RESULT 1462
ID   ADO09827 standard; protein; 681 AA.
DE   Hamster SGLT homologue protein SEQ ID NO:50.
PN   WO2004039405-A1.
PD   13-MAY-2004.
PA   (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity   24.5%; Score 69.5; DB 8; Length 681;
RESULT 1463
ID   ABU41908 standard; protein; 695 AA.
DE   Protein encoded by Prokaryotic essential gene #27435.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity   24.3%; Score 69.5; DB 6; Length 695;
RESULT 1464
ID   ADJ48367 standard; protein; 764 AA.
DE   Maize oil-associated gene protein #26.
PN   US2004025202-A1.
PD   05-FEB-2004.
PA   (LAUR/) LAURIE C C.
PA   (RAVA/) RAVANELLO M.
PA   (SAVA/) SAVAGE T.
PA   (LEDE/) LEDEAUX J R.
PA   (ROGE/) ROGERS J A.
Query Match
Best Local Similarity   21.0%; Score 69.5; DB 8; Length 764;
RESULT 1465
ID   ABU43821 standard; protein; 801 AA.
DE   Protein encoded by Prokaryotic essential gene #29348.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity   19.9%; Score 69.5; DB 6; Length 801;
RESULT 1466
ID   AAY70245 standard; protein; 805 AA.
DE   Human Polycystin-L protein.
PN   WO20012046-A2.
PD   09-MAR-2000.
PA   (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match
Best Local Similarity   19.3%; Score 69.5; DB 3; Length 805;
RESULT 1467
ID   ABB98140 standard; protein; 863 AA.
DE   Human PMMM Incyte ID 7484157CD1.
PN   WO200246383-A2.
PD   13-JUN-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity   20.4%; Score 69.5; DB 5; Length 863;
RESULT 1468
ID   AAY96168 standard; protein; 877 AA.
DE   Saccharomyces cerevisiae OPT protein YPR194C.
PN   WO2005052162-A2.
PD   08-SEP-2000.
PA   (UYTE-) UNIV TENNESSEE RES CORP.

RESULT 1469
ID ADS44117 standard; protein; 877 AA.
DE Bacterial polypeptide #22547.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (BECK/) BECKER J M.
PA (HAUS/) HAUSER M.
PA (DONH/) DONHARDT A.
PA (BARN/) BARNES D.
PA (GOLD/) GOLDMAN B S.
PA (CHEN/) CHEN X.
PA (SLAT/) SLATER S C.
PA (HINK/) HINKLE G J.
PA (CAOY/) CAO Y.
Best Local Similarity 22.7%; Score 69.5; Pred. No. 2.5e+02;
Query Match 5.8%; Score 69.5; DB 3; Length 877;

RESULT 1470
ID AAG70761 standard; protein; 881 AA.
DE S cerevisiae apoptosis associated protein YJL197W.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Best Local Similarity 22.7%; Score 69.5; Pred. No. 2.5e+02;
Query Match 5.8%; Score 69.5; DB 8; Length 881;

RESULT 1471
ID ADZ26338 standard; protein; 913 AA.
DE Mouse hypoxia-responsive gene CNGM0002 protein.
PN WO2005033293-A2.
PD 14-APR-2005.
PA (CENZ) CENTOCOR INC.
Best Local Similarity 24.4%; Score 69.5; Pred. No. 2.5e+02;
Query Match 5.8%; Score 69.5; DB 4; Length 913;

RESULT 1472
ID ABU16635 standard; protein; 1010 AA.
DE Protein encoded by Prokaryotic essential gene #2162.
PN WO200227183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity 18.9%; Score 69.5; Pred. No. 2.6e+02;
Query Match 5.8%; Score 69.5; DB 9; Length 1010;

RESULT 1473
ID ADA34462 standard; protein; 1028 AA.
DE Acinetobacter baumannii protein #1623.
PN US6566958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity 24.7%; Score 69.5; Pred. No. 3e+02;
Query Match 5.8%; Score 69.5; DB 6; Length 1028;

RESULT 1474
ID AAW25671 standard; protein; 1684 AA.
DE hABC3 protein.
PN WO9702346-A2.
PD 23-JAN-1997.
PA (GENZ) GENZYME CORP.
Best Local Similarity 24.7%; Score 69.5; Pred. No. 3.1e+02;
Query Match 5.8%; Score 69.5; DB 6; Length 1684;

RESULT 1475
ID AAW46761 standard; protein; 1684 AA.
DE Amino acid sequence of human ATP binding cassette transporter.
PN WO9748797-A1.
PD 24-DEC-1997.
PA (GENZ) GENZYME CORP.
Best Local Similarity 20.3%; Score 69.5; Pred. No. 6.1e+02;
Query Match 5.8%; Score 69.5; DB 2; Length 1684;

RESULT 1476
ID AAW46771 standard; protein; 1704 AA.
DE Amino acid sequence of human ATP binding cassette transporter.
PN WO9748797-A1.
PD 24-DEC-1997.
PA (GENZ) GENZYME CORP.
Best Local Similarity 20.3%; Score 69.5; Pred. No. 6.1e+02;
Query Match 5.8%; Score 69.5; DB 2; Length 1704;

RESULT 1477
ID ABP52094 standard; protein; 1704 AA.
DE Homo sapiens ABC transporter ABCA3 protein SEQ ID NO:46.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Best Local Similarity 20.3%; Score 69.5; Pred. No. 6.2e+02;
Query Match 5.8%; Score 69.5; DB 5; Length 1704;

RESULT 1478
ID ADJ70414 standard; protein; 1704 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2220.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Best Local Similarity 20.3%; Score 69.5; Pred. No. 6.2e+02;
Query Match 5.8%; Score 69.5; DB 7; Length 1704;

RESULT 1479
ID ADL61289 standard; protein; 1704 AA.
DE Human ATP-binding cassette subfamily A (ABC1) member 3 protein.
PN WO200400583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity 20.3%; Score 69.5; Pred. No. 6.2e+02;
Query Match 5.8%; Score 69.5; DB 8; Length 1704;

RESULT 1480
ID ADY70428 standard; protein; 1704 AA.
DE Human beta-APP, ATP-binding cassette, subfamily A, member 3.
PN WO2005023858-A1.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Best Local Similarity 20.3%; Score 69.5; Pred. No. 6.2e+02;
Query Match 5.8%; Score 69.5; DB 9; Length 1704;

RESULT 1481
ID ADY70716 standard; protein; 1704 AA.
DE Human nicastrin-complex, ATP-binding cassette family A member 3 protein.
PN WO2005023833-A2.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Best Local Similarity 20.3%; Score 69.5; Pred. No. 6.2e+02;
Query Match 5.8%; Score 69.5; DB 9; Length 1704;

RESULT 1482
ID ADB09274 standard; protein; 154 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:3214.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Best Local Similarity 20.3%; Score 69; Pred. No. 25;
Query Match 5.8%; Score 69; DB 6; Length 154;

RESULT 1483
ID ADK16543 standard; protein; 178 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #247.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Best Local Similarity 27.3%; Score 69; Pred. No. 31;
Query Match 5.8%; Score 69; DB 8; Length 178;

RESULT 1484
ID AAU65589 standard; protein; 191 AA.
DE Propionibacterium acnes immunogenic protein #26485.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity 23.3%; Score 69; Pred. No. 34;
Query Match 5.8%; Score 69; DB 4; Length 191;

RESULT 1485
ID ABM62108 standard; protein; 191 AA.
DE Propionibacterium acnes permease/transporter-related polypeptide #26784.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity 26.6%; Score 69; Pred. No. 34;
Query Match 5.8%; Score 69; DB 6; Length 191;

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RESULT 1486
Query Match
Best Local Similarity    26.6%;   Pred. No. 34;
ID   AAW38633 standard; protein; 193 AA.
DE   S. pneumoniae LpPLC protein.
PN   WO9743303-A1.
PD   20-NOV-1997.
PA   (SMK ) SMITHKLINE BEECHAM CORP.
PA   (SMK ) SMITHKLINE BEECHAM PLC.
PN   WO20294868-A2.
PD   28-NOV-2002.

RESULT 1487
Query Match
Best Local Similarity    28.3%;   Pred. No. 34;   Score 69;   DB 2;   Length 193;
ID   AAB21047 standard; protein; 214 AA.
DE   Human nucleic acid-binding protein, NuABP-51.
PN   WO20044900-A2.
PD   03-AUG-2000.
PA   (INCY-) INCYTE PHARM INC.

RESULT 1488
Query Match
Best Local Similarity    24.7%;   Pred. No. 40;   Score 69;   DB 3;   Length 214;
ID   ABP58238 standard; protein; 214 AA.
DE   Human ovary-specific O1-236 (NPM2) protein.
PN   WO200288314-A2.
PD   07-NOV-2002.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.

RESULT 1489
Query Match
Best Local Similarity    24.7%;   Pred. No. 40;   Score 69;   DB 6;   Length 214;
ID   ADJ63172 standard; protein; 214 AA.
DE   Human nucleoplasmin (Npm2) protein.
PN   WO2003091400-A2.
PD   06-NOV-2003.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.

RESULT 1490
Query Match
Best Local Similarity    24.7%;   Pred. No. 40;   Score 69;   DB 7;   Length 214;
ID   ADM03849 standard; protein; 214 AA.
DE   Human protein of the invention SEQ ID NO:2534.
PN   EP147046-A1.
PD   24-SEP-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.

RESULT 1491
Query Match
Best Local Similarity    24.7%;   Pred. No. 46;   Score 69;   DB 8;   Length 239;
ID   ADN46858 standard; protein; 239 AA.
DE   Thermococcus kodakaraensis KOD1 protein sequence SeqID736.
PN   WO2004022736-A1.
PD   18-MAR-2004.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.

RESULT 1492
Query Match
Best Local Similarity    23.5%;   Pred. No. 64;   Score 69;   DB 8;   Length 301;
ID   ADT57286 standard; protein; 301 AA.
DE   Plant polypeptide, SEQ ID 7363.
PN   US2004216190-A1.
PD   28-OCT-2004.
PA   (KOVA/) KOVALIC D K.

RESULT 1493
Query Match
Best Local Similarity    20.3%;   Pred. No. 65;   Score 69;   DB 8;   Length 306;
ID   ADT98603 standard; protein; 306 AA.
DE   Human mutant GPR10 protein.
PN   US2004216177-A1.
PD   28-OCT-2004.
PA   (SAKA ) OTSUKA PHARM CO LTD.

RESULT 1494
Query Match
Best Local Similarity    21.8%;   Pred. No. 65;   Score 69;   DB 8;   Length 337;
ID   ABM69545 standard; protein; 337 AA.
DE   Photorhabdus luminescens protein sequence #2642.
PN   WO20294867-A2.
PD   28-NOV-2002.

RESULT 1495
Query Match
Best Local Similarity    19.8%;   Pred. No. 74;   Score 69;   DB 6;   Length 350;
ID   ABM72781 standard; protein; 350 AA.
DE   Staphylococcus aureus protein #2021.
PN   WO20294868-A2.
PD   28-NOV-2002.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
PA   (INSP ) INST PASTEUR.

RESULT 1496
Query Match
Best Local Similarity    20.5%;   Pred. No. 78;   Score 69;   DB 3;   Length 356;
ID   AAG04120 standard; protein; 356 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 27.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (CHIR-) CHIRON SPA.

RESULT 1497
Query Match
Best Local Similarity    21.0%;   Pred. No. 80;   Score 69;   DB 2;   Length 370;
ID   AAR91218 standard; protein; 370 AA.
DE   Human pituitary G-protein coupled receptor protein.
PN   WO9605302-A1.
PD   22-FEB-1996.
PA   (TAKE ) TAKEDA CHEM IND LTD.

RESULT 1498
Query Match
Best Local Similarity    21.8%;   Pred. No. 85;   Score 69;   DB 3;   Length 370;
ID   AAW31379 standard; protein; 370 AA.
DE   Human G protein-coupled receptor protein from phGR3.
PN   WO9724436-A2.
PD   10-JUL-1997.
PA   (TAKE ) TAKEDA CHEM IND LTD.

RESULT 1499
Query Match
Best Local Similarity    21.8%;   Pred. No. 85;   Score 69;   DB 2;   Length 370;
ID   AAW95181 standard; protein; 370 AA.
DE   Human G-protein coupled receptor polypeptide.
PN   WO9849295-A1.
PD   05-NOV-1998.
PA   (TAKE ) TAKEDA CHEM IND LTD.

RESULT 1500
Query Match
Best Local Similarity    21.8%;   Pred. No. 85;   Score 69;   DB 2;   Length 370;
ID   AAW97221 standard; peptide; 370 AA.
DE   Human pituitary-derived G protein-coupled receptor protein.
PN   WO9858962-A1.
PD   30-DEC-1998.
PA   (TAKE ) TAKEDA CHEM IND LTD.
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OM protein - protein search, using sw model

GenCore version 5.1.8
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Run on: May 12, 2006, 20:47:47 ; Search time 46 Seconds
(without alignments)
420.568 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
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Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 572060

Searched: 572060 seqs, 82675679 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	669.5	56.0	176	2	US-10-104-047-2567	Sequence 2567, Ap
2	664	55.6	445	1	US-08-691-814B-6	Sequence 6, Appli
3	85.5	7.2	449	2	US-09-949-016-8594	Sequence 8594, Ap
4	82.5	6.9	341	1	US-08-846-762-92	Sequence 92, Appl
5	80.5	6.7	350	2	US-09-489-039A-9711	Sequence 9711, Ap
6	80.5	6.7	891	2	US-10-226-629A-16	Sequence 16, Appl
7	80.5	6.7	406	2	US-09-171-699-4	Sequence 4, Appli
8	79.5	6.7	406	4	PCT-US94-02107-2	Sequence 2, Appli
9	79.5	6.7	723	2	US-09-976-594-503	Sequence 503, App
10	79.5	6.6	221	2	US-09-270-767-41033	Sequence 41033, A
11	78.5	6.6	221	2	US-09-270-767-56249	Sequence 56249, A
12	78.5	6.6	766	2	US-09-724-653-2	Sequence 2, Appli
13	78.5	6.6	766	2	US-09-724-653-14	Sequence 14, Appl
14	78.5	6.6	766	2	US-09-724-653-15	Sequence 15, Appl
15	78	6.5	228	2	US-09-248-796A-20444	Sequence 20444, A
16	78	6.5	251	2	US-09-270-767-43373	Sequence 43373, A
17	78	6.5	355	2	US-08-833-752-9	Sequence 9, Appl
18	78	6.5	355	2	US-09-938-719-9	Sequence 9, Appl
19	78	6.5	355	2	US-09-939-226B-9	Sequence 9, Appl
20	78	6.5	355	2	US-09-938-703B-9	Sequence 9, Appl
21	77.5	6.5	892	2	US-10-226-629A-15	Sequence 15, Appl
22	77	6.5	353	2	US-08-466-103A-14	Sequence 14, Appl
23	77	6.4	353	2	US-09-280-420-2	Sequence 2, Appli
24	77	6.4	353	2	US-09-479-195-2	Sequence 2, Appli
25	76.5	6.4	435	2	US-09-489-039A-12344	Sequence 12344, A
26	76.5	6.4	494	1	US-08-464-340A-4	Sequence 4, Appli
27	76.5	6.4	494	4	PCT-US94-08449A-4	Sequence 4, Appli
28	76.5	6.4	555	2	US-10-104-047-2011	Sequence 2011, Ap
29	76	6.4	195	2	US-09-134-000C-5992	Sequence 5992, Ap
30	76	6.4	593	2	US-09-720-317A-22	Sequence 22, Appl
31	75.5	6.4	263	2	US-09-583-110-3148	Sequence 3148, Ap
32	75.5	6.3	264	2	US-09-769-787-119	Sequence 119, App
33	75.5	6.3	352	2	US-09-107-433-4877	Sequence 4877, Ap
34	75.5	6.3	352	2	US-09-492-709A-293	Sequence 293, App
35	75.5	6.3	397	2	US-09-248-796A-14258	Sequence 14258, A
36	75.5	6.3	397	2	US-09-721-870-105	Sequence 105, App
37	75.5	6.3	433	2	US-09-721-870-107	Sequence 107, App
38	75.5	6.3	471	1	US-08-477-451-20	Sequence 20, Appl
39	75.5	6.3	499	2	US-09-328-352-5465	Sequence 5465, Ap
40	75	6.3	467	2	US-09-134-000C-4375	Sequence 4375, Ap
41	75	6.3	549	1	US-10-104-047-2866	Sequence 2866, Ap
42	75	6.3	1131	1	US-08-153-848-32	Sequence 32, Appl
43	74.5	6.2	355	1	US-08-153-848-28	Sequence 28, Appl
44	74.5	6.2	355	2	US-09-299-843A-28	Sequence 28, Appl
45	74.5	6.2	355	2	US-09-299-843A-32	Sequence 32, Appl
46	74.5	6.2	355	2	US-09-088-337B-28	Sequence 28, Appl
47	74.5	6.2	355	2	US-09-088-337B-32	Sequence 32, Appl
48	74.5	6.2	355	2	US-09-170-496D-130	Sequence 130, App
49	74.5	6.2	355	2	US-09-170-496D-232	Sequence 232, App
50	74.5	6.2	355	1	US-09-917-254-68	Sequence 68, Appl
51	74.5	6.2	355	4	PCT-US93-11153-28	Sequence 28, Appl
52	74.5	6.2	355	4	PCT-US93-11153-32	Sequence 32, Appl
53	74.5	6.2	355	2	US-09-328-352-8165	Sequence 8165, Ap
54	74.5	6.2	471	2	US-09-543-681A-7579	Sequence 7579, A
55	74.5	6.2	471	2	US-09-543-681A-2662	Sequence 2662, A
56	74.5	6.2	471	1	US-09-032-742-2	Sequence 2, Appli
57	74.5	6.2	471	2	US-09-032-742-11	Sequence 11, Appl
58	74.5	6.1	471	2	US-09-032-742-14	Sequence 14, Appl
59	74.5	6.1	471	2	US-09-032-742-17	Sequence 17, Appl
60	74.5	6.2	940	2	US-09-145-864-4	Sequence 4, Appli
61	74	6.2	154	2	US-09-902-940-11488	Sequence 11488, A
62	74	6.2	332	1	US-07-996-772A-11	Sequence 11, Appl
63	74	6.2	350	1	US-08-466-103A-12	Sequence 12, Appl
64	74	6.2	353	1	US-08-896-765-6	Sequence 6, Appli
65	74	6.2	680	2	US-09-248-796A-15089	Sequence 15089, A
66	73.5	6.2	312	2	US-09-543-681A-6267	Sequence 6267, A
67	73.5	6.2	400	2	US-09-902-940-11488	Sequence 11488, A
68	73.5	6.2	3033	9	US-07-925-695-9	Sequence 9, Appli
69	73	6.1	199	2	US-09-107-532A-6773	Sequence 6773, A
70	73	6.1	272	2	US-09-903-456-75	Sequence 75, Appl
71	73	6.1	364	2	US-09-077-675A-16	Sequence 16, Appl
72	73	6.1	364	2	US-09-077-674-16	Sequence 16, Appl
73	73	6.1	364	2	US-09-762-661A-6	Sequence 6, Appli
74	73	6.1	364	2	US-09-743-475-5	Sequence 5, Appli
75	73	6.1	377	2	US-09-949-016-7475	Sequence 7475, A
76	73	6.1	364	2	US-08-936-165A-533	Sequence 533, App
77	73	6.1	494	2	US-09-489-039A-9817	Sequence 9817, Ap
78	72.5	6.1	501	2	US-08-785-431-4	Sequence 4, Appli
79	73	6.1	746	1	US-08-785-431-4	Sequence 4, Appli
80	73	6.1	746	1	US-08-785-431-4	Sequence 4, Appli
81	73	6.1	788	1	US-09-785-431-2	Sequence 2, Appli
82	73	6.1	788	1	US-08-785-431-2	Sequence 2, Appli
83	72.5	6.1	312	2	US-09-205-048-20385	Sequence 20385, A
84	72.5	6.1	353	2	US-09-248-796A-20385	Sequence 20385, A
85	72.5	6.1	359	2	US-09-134-000C-5562	Sequence 5562, Appl
86	72.5	6.1	448	1	US-09-134-000C-5442	Sequence 5442, Appl
87	72.5	6.1	448	2	US-08-811-897A-16	Sequence 16, Appl
88	72.5	6.1	448	2	US-08-855-213-16	Sequence 16, Appl
89	72.5	6.1	476	2	US-09-201-474-16	Sequence 16, Appl
90	72.5	6.1	476	2	US-08-811-897A-14	Sequence 14, Appl
91	72.5	6.1	476	2	US-08-855-213-14	Sequence 14, Appl
92	72.5	6.1	476	1	US-09-201-474-14	Sequence 14, Appl
93	72.5	6.1	485	2	US-08-811-897A-17	Sequence 17, Appl
94	72.5	6.1	485	2	US-08-855-213-17	Sequence 17, Appl
95	72.5	6.1	485	2	US-09-201-474-17	Sequence 17, Appl
96	72.5	6.1	513	2	US-08-811-897A-15	Sequence 15, Appl
97	72.5	6.1	513	2	US-08-855-213-15	Sequence 15, Appl
98	72	6.0	513	2	US-09-201-474-15	Sequence 15, Appl
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106	72	6.0	2307	2	US-09-919-901-2	Sequence 2, Appli
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111	72	6.0	2307	2	US-10-191-966-9	Sequence 9, Appli
112	72	6.0	2307	2	US-08-785-928-1	Sequence 16, Appli
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114	71.5	6.0	342	2	US-08-466-103A-4	Sequence 17, Appli
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127	71	5.9	470	2	US-10-176-255-25	Sequence 25, Appli
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131	71	5.9	471	1	US-08-216-594-8	Sequence 8, Appli
132	71	5.9	471	1	US-08-542-358-7	Sequence 8, Appli
133	71	5.9	471	2	US-08-018-351-7	Sequence 7, Appli
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135	71	5.9	471	2	US-09-145-864-2	Sequence 8, Appli
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137	71	5.9	471	2	US-10-092-138A-28	Sequence 122, App
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154	70.5	5.9	388	2	US-08-240-783B-4	Sequence 4, Appli
155	70.5	5.9	390	2	US-09-661-758A-6	Sequence 6, Appli
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185	70	5.9	333	2	US-09-170-496D-172	Sequence 172, Appl
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191	70	5.9	425	2	US-09-107-532A-6574	Sequence 6574, Ap
192	70	5.9	461	2	US-09-583-110-3842	Sequence 3842, Ap
193	70	5.9	470	2	US-09-107-433-3722	Sequence 3722, Ap
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195	70	5.9	471	2	US-10-327-189-4	Sequence 4, Appli
196	70	5.9	198	2	US-09-521-195B-3	Sequence 3, Appli
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207	69.5	5.8	557	2	US-09-540-236-2346	Sequence 2346, Ap
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212	69.5	5.8	599	1	US-09-134-001C-5039	Sequence 5039, Ap
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214	69.5	5.8	610	2	US-09-949-016-9494	Sequence 9494, Ap
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216	69.5	5.8	663	2	US-09-165-396-5	Sequence 5, Appli
217	69.5	5.8	676	2	US-09-328-352-5749	Sequence 5749, Ap
218	69.5	5.8	676	2	US-08-665-259-25	Sequence 25, Appl
219	69.5	5.8	877	2	US-09-762-500-25	Sequence 25, Appl
220	69.5	5.8	1028	1	US-08-762-500-75	Sequence 75, Appl
221	69.5	5.8	1684	2	US-09-032-438C-120	Sequence 120, Appl
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224	69	5.8	340	2	US-09-248-796A-15237	Sequence 15237, A
225	69	5.8	370	2	US-08-513-974B-26	Sequence 26, Appl
226	69	5.8	370	2	US-08-513-974B-323	Sequence 323, App
227	69	5.8	370	2	US-09-172-353-5	Sequence 5, Appli
228	69	5.8	370	2	US-08-776-971-104	Sequence 104, App
229	69	5.8	370	2	US-08-776-971-104	Sequence 104, App
230	69	5.8	370	2	US-09-799-955-5	Sequence 5, Appli
231	69	5.8	370	2	US-09-461-436B-26	Sequence 26, Appl
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233	69	5.8	370	2	US-09-576-290-104	Sequence 104, App
234	69	5.8	370	2	US-09-716-147-21	Sequence 21, Appl
235	69	5.8	370	2	US-09-716-147-104	Sequence 104, App
236	69	5.8	388	2	US-09-492-709A-378	Sequence 378, App
237	69	5.8	472	2	US-09-489-039A-8418	Sequence 8418, A
238	69	5.8	552	2	US-09-270-767-45540	Sequence 45540, A
239	69	5.8	681	2	US-09-543-681A-5453	Sequence 5453, A
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254	68.5	5.7	383	1	US-08-196-989B-4	Sequence 4, Appli
255	68.5	5.7	383	2	US-08-760-936-4	Sequence 4, Appli
256	68.5	5.7	417	2	US-09-225-024-4	Sequence 4, Appli
257	68.5	5.7	420	1	US-09-134-000C-5002	Sequence 5002, Ap
258	68.5	5.7	437	2	US-09-328-352-5102	Sequence 5102, Ap
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260	68.5	5.7	444	2	US-09-580-734-15	Sequence 15, Appl
261	68.5	5.7	444	2	US-08-374-009-15	Sequence 15, Appl
262	68.5	5.7	444	2	US-09-191-724-15	Sequence 15, Appl
263	68.5	5.7	444	2	US-09-631-603-11	Sequence 11, Appl
264	68.5	5.7	444	2	US-08-811-897A-22	Sequence 22, Appl
265	68.5	5.7	448	1	US-09-631-603-22	Sequence 22, Appl
266	68.5	5.7	448	2	US-08-855-213-22	Sequence 22, Appl
267	68.5	5.7	448	2	US-08-811-897A-22	Sequence 22, Appl
268	68.5	5.7	468	2	US-09-201-474-22	Sequence 22, Appl
269	68.5	5.7	468	2	US-09-826-509-553	Sequence 553, Appl
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273	68.5	5.7	476	1	US-08-855-213-26	Sequence 26, Appl
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279	68.5	5.7	476	1	US-08-811-897A-23	Sequence 23, Appl
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297	68.5	5.7	188	1	US-09-603-208A-152	Sequence 152, App
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305	68.5	5.7	346	2	US-10-314-048A-14	Sequence 14, Appl
306	68.5	5.7	346	2	US-10-314-048A-88	Sequence 88, Appl
307	68.5	5.7	346	2	US-09-012-988A-2	Sequence 2, Appl
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317	68	5.7	373	2	US-09-489-039A-10869	Sequence 10869, A
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324	68	5.7	471	2	US-08-716-873-28	Sequence 28, Appl
325	68	5.7	471	2	US-09-368-431-8	Sequence 8, Appl
326	68	5.7	471	2	US-09-368-431-28	Sequence 28, Appl
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328	68	5.7	471	2	US-08-440-006-14	Sequence 14, Appl
329	68	5.7	471	2	US-09-447-223-14	Sequence 14, Appl
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368	67.5	5.7	2621	1	US-08-904-686A-36	Sequence 36, Appl
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405	67	5.6	153	2	US-09-438-185A-314	Sequence 314, App
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408	67	5.6	184	2	US-09-830-230A-150	Sequence 150, App
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546	66	5.5	381	2	US-09-518-383-18	Sequence 18, Appl
547	66	5.5	381	2	PCT-US96-10618-4	Sequence 4, Appl
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549	66	5.5	412	2	US-09-138-701-59	Sequence 59, Appl
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606	65	5.5	282	2	US-09-252-991A-19489	Sequence 19489, A
607	65	5.5	311	2	US-09-107-532A-5538	Sequence 5538, Ap
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610	65	5.4	362	2	US-09-485-648-6	Sequence 6, Appli
611	65	5.4	362	2	US-09-503-565-6	Sequence 6, Appli

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612	65	5.4	362	2	US-09-485-649-6	Sequence 6, Appli
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618	65	5.4	415	2	US-09-374-009-2	Sequence 2, Appli
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621	65	5.4	415	2	US-09-799-978-4	Sequence 4, Appli
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623	65	5.4	415	2	US-09-826-509-483	Sequence 483, App
624	65	5.4	432	2	US-09-710-279-780	Sequence 780, App
625	65	5.4	441	2	US-09-540-236-2016	Sequence 2016, Ap
626	65	5.4	461	1	US-08-672-814D-2	Sequence 2, Appl
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628	65	5.4	461	2	US-08-282-218A-2	Sequence 2, Appl
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632	65	5.4	490	2	US-08-612-973-36	Sequence 36, Appl
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634	65	5.4	491	2	US-09-181-339-7	Sequence 7, Appli
635	65	5.4	516	2	US-09-949-016-11239	Sequence 11239, A
636	65	5.4	637	2	US-09-543-681A-5869	Sequence 5869, Ap
637	65	5.4	692	2	US-08-612-973-48	Sequence 48, Appl
638	65	5.4	692	2	US-08-927-597-48	Sequence 48, Appl
639	65	5.4	692	2	US-08-612-973-50	Sequence 50, Appl
640	65	5.4	809	2	US-08-927-597-50	Sequence 50, Appl
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642	65	5.4	809	2	US-09-252-991A-21511	Sequence 21511, A
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647	64.5	5.4	263	1	US-09-328-532-7066	Sequence 7066, Ap
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649	64.5	5.4	311	2	US-09-248-796A-13216	Sequence 13216, A
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683	64.5	5.4	486	2	US-09-291-922-10	Sequence 10, Appl
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692	64.5	5.4	557	2	US-09-805-694B-16	Sequence 16, Appl
693	64.5	5.4	557	2	US-09-521-195B-27	Sequence 27, Appl
694	64.5	5.4	567	2	US-09-798-743-3	Sequence 3, Appl
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736	64.5	5.4	504	2	US-09-583-447A-4	Sequence 4, Appli
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773	63.5	5.3	275	1	PCT-US93-08528-66	Sequence 66, Appl
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776	63.5	5.3	308	2	US-09-852-156-6	Sequence 6, Appli
777	63.5	5.3	337	2	US-09-852-156-4	Sequence 4, Appli
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780	63.5	5.3	342	2	US-09-116-498-6	Sequence 6, Appli
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813	63.5	5.3	489	2	US-09-997-333-138	Sequence 138, App
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857	63	5.3	415	2	US-09-191-724-13	Sequence 13, Appl
858	63	5.3	415	2	US-09-799-978-22	Sequence 22, Appl
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872	63	5.3	509	2	US-08-890-980-2	Sequence 2, Appli
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881	63	5.3	943	2	US-10-314-048A-104	Sequence 104, App
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886	63	5.3	2985	2	US-10-259-275-40	Sequence 40, Appl
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903	62.5	5.3	255	2	US-09-997-333-287	Sequence 287, App
904	62.5	5.2	255	2	US-09-992-598-287	Sequence 287, App
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1133	61	5.1	200	2	US-09-710-279-1242	Sequence 1242, Ap
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1136	61	5.1	207	2	US-09-559-397A-13	Sequence 13, Appl
1137	61	5.1	209	2	US-09-252-991A-11	Sequence 11, Appl
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1141	61	5.1	241	2	US-09-489-039A-8397	Sequence 8397, Ap
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1156	61	5.1	302	2	US-09-311-731A-173	Sequence 173, App
1157	61	5.1	338	2	US-09-107-532A-6222	Sequence 6222, Ap
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1188	61	5.1	915	2	US-09-107-532A-3714	Sequence 3714, Ap
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1197	61	5.1	2864	2	US-08-488-446-394	Sequence 394, Appl
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1226	60.5	5.1	200	4	US-09-393-634-17	Sequence 17, Appl
1227	60.5	5.1	207	2	PCT-US95-09927-9	Sequence 9, Appl
1228	60.5	5.1	222	2	US-08-811-519-18	Sequence 18, Appl
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1236	60.5	5.1	285	2	PCT-US93-08528-78	Sequence 78, Appl
1237	60.5	5.1	296	2	US-09-540-236-2856	Sequence 2856, Ap
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1242	60.5	5.1	342	2	US-09-721-341-9	Sequence 9, Appl
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1263	60.5	5.1	473	1	US-09-830-230A-90	Sequence 90, Appl
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1268	60.5	5.1	487	2	US-10-093-317-8	Sequence 8, Appli

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1311	60.5	5.1	206	2	US-09-461-436B-27	Sequence 27, Appl
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1319	60.5	5.1	223	2	US-08-776-971-102	Sequence 102, App
1320	60.5	5.1	223	2	US-08-776-971-108	Sequence 108, App
1321	60.5	5.1	223	2	US-09-576-290-100	Sequence 100, App
1322	60.5	5.1	223	2	US-09-576-290-102	Sequence 102, App
1323	60.5	5.1	223	2	US-09-576-290-108	Sequence 108, App
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1341	60	5.0	328	2	US-09-543-681A-5252	Sequence 5252, Ap

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1354	60	5.0	382	2	US-09-134-001C-4483	Sequence 4483, Ap
1355	60	5.0	387	2	US-08-990-379-8	Sequence 8, Appli
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1365	60	5.0	421	1	US-08-484-040-3	Sequence 3, Appli
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1375	60	5.0	502	2	US-09-134-000C-5949	Sequence 5949, Ap
1376	60	5.0	521	2	US-09-538-092-1330	Sequence 1330, Ap
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1378	60	5.0	526	2	US-09-949-016-11505	Sequence 11505, A
1379	60	5.0	568	1	US-09-538-092-10896	Sequence 10896, A
1380	60	5.0	587	2	US-08-893-852A-4	Sequence 4, Appli
1381	60	5.0	587	2	US-08-818-2	Sequence 1130, Ap
1382	60	5.0	590	2	US-09-052-753B-2	Sequence 2, Appli
1383	60	5.0	590	2	US-09-938-782A-2	Sequence 2, Appli
1384	60	5.0	590	2	US-08-578-441-2	Sequence 2, Appli
1385	60	5.0	626	1	US-08-630-524-2	Sequence 2, Appli
1386	60	5.0	626	2	US-07-938-782A-2	Sequence 2, Appli
1387	60	5.0	626	4	US-09-487-588B-242	Sequence 2, Appli
1388	60	5.0	630	2	US-09-602-787A-548	Sequence 548, App
1389	60	5.0	630	2	US-09-134-001C-5661	Sequence 5661, Ap
1390	60	5.0	667	1	US-08-718-661-2	Sequence 2, Appli
1391	60	5.0	667	2	US-09-307-143-6	Sequence 6, Appli
1392	60	5.0	724	2	US-09-328-352-4442	Sequence 4442, Ap
1393	60	5.0	730	2	US-09-585-858-9	Sequence 9, Appli
1394	60	5.0	734	2	US-09-328-352-4442	Sequence 4442, Ap
1395	60	5.0	734	2	US-09-585-858-9	Sequence 9, Appli
1396	60	5.0	756	2	US-10-270-878-9	Sequence 9, Appli
1397	60	5.0	770	2	US-09-949-016-7042	Sequence 7042, Ap
1398	60	5.0	770	2	US-09-252-991A-28510	Sequence 28510, A
1399	60	5.0	797	2	US-09-949-016-6657	Sequence 6657, Ap
1400	60	5.0	908	2	US-09-855-146-2	Sequence 2, App
1401	60	5.0	1068	2	US-09-487-588B-242	Sequence 242, App
1402	60	5.0	1137	2	US-09-252-991A-24829	Sequence 24829, A
1403	60	5.0	1156	2	US-09-198-452A-171	Sequence 171, App
1404	60	5.0	1179	2	US-09-949-016-10545	Sequence 10545, A
1405	60	5.0	1296	1	US-08-857-636-60	Sequence 60, Appl
1406	60	5.0	1296	2	US-09-540-440-60	Sequence 60, Appl
1407	60	5.0	1447	2	US-08-656-055-19	Sequence 19, Appl
1408	60	5.0	1447	2	US-09-268-140-5	Sequence 5, Appl
1409	60	5.0	1447	2	US-08-918-658-19	Sequence 19, Appl
1410	60	5.0	1447	2	US-08-918-658-19	Sequence 19, Appl
1411	60	5.0	1447	2	US-09-724-631-19	Sequence 19, Appl
1412	60	5.0	1447	2	US-09-954-032-19	Sequence 6, Appl
1413	60	5.0	1447	2	US-09-807-007-6	Sequence 19, Appl
1414	60	5.0	1447	2	US-09-754-032-19	Sequence 19, Appl

1415	60	5.0	1447	4	PCT-US95-13233-19	Sequence 19, Appl
1416	60	5.0	1562	2	US-09-438-185A-152	Sequence 152, App
1417	60	5.0	1659	2	US-09-487-558B-118	Sequence 118, App
1418	60	5.0	1681	2	US-09-920-653B-3	Sequence 3, Appli
1419	60	5.0	2235	2	US-09-032-438C-6	Sequence 6, Appli
1420	60	5.0	2273	2	US-10-226-629A-13	Sequence 13, Appl
1421	60	5.0	2940	2	US-09-032-438C-3	Sequence 3, Appli
1422	60	5.0	3011	1	US-08-453-552-2	Sequence 2, Appli
1423	60	5.0	3011	1	US-08-710-637-2	Sequence 2, Appli
1424	60	5.0	3011	4	PCT-US93-00907-2	Sequence 2, Appli
1425	60	5.0	151	2	US-09-328-352-4208	Sequence 4208, Ap
1426	59.5	5.0	159	2	US-09-248-796A-27840	Sequence 27840, A
1427	59.5	5.0	161	2	US-09-270-767-36990	Sequence 36990, A
1428	59.5	5.0	161	2	US-09-270-767-52207	Sequence 52207, A
1429	59.5	5.0	195	1	US-08-467-822-44	Sequence 44, Appl
1430	59.5	5.0	195	2	US-08-211-312-3	Sequence 3, Appli
1431	59.5	5.0	195	2	US-08-472-285-3	Sequence 3, Appli
1432	59.5	5.0	195	2	US-09-107-383-10	Sequence 10, Appl
1433	59.5	5.0	195	2	US-08-466-248-44	Sequence 44, Appl
1434	59.5	5.0	195	2	US-09-107-532A-44	Sequence 44, Appl
1435	59.5	5.0	195	2	US-08-472-929-3	Sequence 3, Appli
1436	59.5	5.0	195	2	US-09-643-914-10	Sequence 10, Appl
1437	59.5	5.0	195	2	US-09-742-361A-10	Sequence 10, Appl
1438	59.5	5.0	199	2	US-08-478-316-37	Sequence 37, Appl
1439	59.5	5.0	199	2	US-09-019-793A-37	Sequence 37, Appl
1440	59.5	5.0	199	2	US-09-601-326-37	Sequence 37, Appl
1441	59.5	5.0	199	2	US-09-248-796A-16080	Sequence 16080, A
1442	59.5	5.0	209	2	US-09-813-453B-21	Sequence 21, Appl
1443	59.5	5.0	220	2	US-09-107-532A-6803	Sequence 6803, Ap
1444	59.5	5.0	232	2	US-09-107-532A-6747	Sequence 6747, Ap
1445	59.5	5.0	247	2	US-09-991-181-303	Sequence 303, App
1446	59.5	5.0	247	2	US-09-990-444-303	Sequence 303, App
1447	59.5	5.0	247	2	US-09-997-333-303	Sequence 303, App
1448	59.5	5.0	247	2	US-09-992-598-303	Sequence 303, App
1449	59.5	5.0	249	2	US-09-328-352-4690	Sequence 4690, Ap
1450	59.5	5.0	268	2	US-09-902-540-14104	Sequence 14104, A
1451	59.5	5.0	275	2	US-09-371-056-10	Sequence 10, Appl
1452	59.5	5.0	280	2	US-09-543-681A-6175	Sequence 6175, Ap
1453	59.5	5.0	281	2	US-09-134-000C-4344	Sequence 4344, Ap
1454	59.5	5.0	293	2	US-09-107-532A-4206	Sequence 4206, Ap
1455	59.5	5.0	295	2	US-09-543-681A-5660	Sequence 5660, Ap
1456	59.5	5.0	300	2	US-09-830-230A-206	Sequence 206, App
1457	59.5	5.0	312	2	US-10-104-047-2478	Sequence 2478, Ap
1458	59.5	5.0	324	2	US-09-902-540-12246	Sequence 12246, A
1459	59.5	5.0	327	2	US-08-926-724-3	Sequence 3, Appli
1460	59.5	5.0	327	2	US-08-904-03-3	Sequence 3, Appli
1461	59.5	5.0	327	2	US-09-540-236-2590	Sequence 2590, Ap
1462	59.5	5.0	341	1	US-08-423-564-5	Sequence 5, Appli
1463	59.5	5.0	350	1	US-08-118-270-41	Sequence 41, Appl
1464	59.5	5.0	350	2	US-09-910-695-8	Sequence 8, Appli
1465	59.5	5.0	350	4	PCT-US93-08528-41	Sequence 41, Appl
1466	59.5	5.0	364	2	US-09-830-230A-205	Sequence 205, App
1467	59.5	5.0	369	2	US-09-543-681A-6725	Sequence 6725, Ap
1468	59.5	5.0	370	2	US-09-134-001C-4166	Sequence 4166, Ap
1469	59.5	5.0	388	2	US-09-222-938A-37	Sequence 37, Appl
1470	59.5	5.0	399	2	US-09-583-110-2855	Sequence 2855, Ap
1471	59.5	5.0	399	2	US-09-107-433-3898	Sequence 3898, Ap
1472	59.5	5.0	431	1	US-08-993-750C-24	Sequence 24, Appl
1473	59.5	5.0	431	2	US-09-234-613-24	Sequence 24, Appl
1474	59.5	5.0	439	1	US-08-853-659A-37	Sequence 37, Appl
1475	59.5	5.0	444	2	US-09-540-236-1993	Sequence 1993, Ap
1476	59.5	5.0	445	2	US-09-710-279-2644	Sequence 2644, Ap
1477	59.5	5.0	447	2	US-09-694-519-9	Sequence 9, Appli
1478	59.5	5.0	491	2	US-09-543-681A-4195	Sequence 4195, Ap
1479	59.5	5.0	593	2	US-09-248-796A-14472	Sequence 14472, A
1480	59.5	5.0	606	2	US-09-107-532A-4683	Sequence 4683, Ap
1481	59.5	5.0	649	2	US-09-134-001C-3891	Sequence 3891, Ap
1482	59.5	5.0	662	2	US-09-252-991A-22861	Sequence 22861, A
1483	59.5	5.0	680	1	US-08-674-351-2	Sequence 2, Appli
1484	59.5	5.0	714	2	US-10-087-402-19	Sequence 19, Appl
1485	59.5	5.0	738	2	US-09-328-355-4315	Sequence 4315, Ap
1486	59.5	5.0	739	1	US-07-803-622E-2	Sequence 2, Appli
1487	59.5	5.0	753	2	US-09-252-991A-17631	Sequence 17631, A
1488	59.5	5.0	832	2	US-10-012-231A-227	Sequence 227, App
1489	59.5	5.0	832	2	US-10-015-389A-227	Sequence 227, App
1490	59.5	5.0	832	2	US-10-006-768A-227	Sequence 227, App
1491	59.5	5.0	832	2	US-10-015-671A-227	Sequence 227, App
1492	59.5	5.0	832	2	US-10-015-393A-227	Sequence 227, App
1493	59.5	5.0	832	2	US-10-011-833A-227	Sequence 227, App
1494	59.5	5.0	832	2	US-10-006-041A-227	Sequence 227, App
1495	59.5	5.0	832	2	US-10-012-064A-227	Sequence 227, App
1496	59.5	5.0	835	2	US-10-538-092-770	Sequence 770, App
1497	59.5	5.0	852	2	US-09-081-385-153	Sequence 153, App
1498	59.5	5.0	852	2	US-09-752-639-153	Sequence 153, App
1499	59.5	5.0	852	2	US-09-712-813-153	Sequence 153, App
1500	59.5	5.0	852	2	US-09-700-354A-153	Sequence 153, App

ALIGNMENTS

RESULT 1
US-10-104-047-2567
; Sequence 2567, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2567
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2567

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  Query Match       56.0%;  Score 669.5;  DB 2;  Length 176;
  Best Local Similarity   87.5%;  Pred. No. 3.9e-69;
  Matches  133;  Conservative   6;  Mismatches  12;  Indels   1;  Gaps   1;

Qy         1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKGISDVRRTFCLFVT 60
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Qy        61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLLIAYAVCRL 120
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Db        61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLLIAYAVCRL 120

Qy       121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAF 152
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Db       121 RHWWAIAVSMPCMSG-SSPPVLVAKSCSQOAW 151
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RESULT 2
US-08-691-814B-6
; Sequence 6, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

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; ZIP: 2000S-3934
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/691,814B
;   FILING DATE: 31-JUL-1996
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/002,183
;   FILING DATE: 09-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Steffe, Eric K.
;   REGISTRATION NUMBER: 36,688
;   REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-371-2600
;   TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 445 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-691-814B-6

Query Match        55.6%;  Score 664;  DB 1;  Length 445;
Best Local Similarity   56.2%;  Pred. No. 6.3e-68;
Matches 135;  Conservative 38;  Mismatches 45;  Indels 22;  Gaps 5;

Qy    1  MNHLP---------EDMENAL------------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV   51
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Db    1  MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSHHLLPPE--------------KRRAISDV   49

Qy   52  RRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVRFKVL   111
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Db   50  RRTFCLFVTFDLLFISLLWIIELNTNTGIRKNLEQEIIQNFKTSFFDIFVLAFPRFSGL   109

Qy  112  ILAYAVCRLRHWWAIALTTTAVTSAFLLAKVILSKLFSQGARFGYVLPIISFILAWIETWFL   171
         :|:|||||||||||||||||||||:|||||||||||||||||:||||||||||:||:|||
Db  110  LLGYAVLQLRHWWIAVTLVSSAAFLIVKVILSELLSKGAFGYLLPIVSFVLAMLETWFL   169

Qy  172  DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESSAGSE-EAEEKQDSEK   229
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Db  170  DFKVLPQEAEEERWLAAQAVAVARGPLLPSGALSEGQFYSPPESFAGSDNESDEEVAGKK   229

RESULT 3
US-09-949-016-8594
; Sequence 8594, Application US/0944016
; Patent No. 6812339
; GENERAL INFORMATION:
;   Patent No. 6812339
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;      WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8594
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8594
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Query Match        7.2%;  Score 85.5;  DB 2;  Length 449;
Best Local Similarity   25.5%;  Pred. No. 0.45;
Matches 38;  Conservative 18;  Mismatches 46;  Indels 47;  Gaps 8;

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Qy  109  KVLILAYAVCRLRHWWAIALTTTAVTSAFLLAKVILSKLFSQGARFGYVLPIISFIL----   163
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Qy  164  ------AWIETWFLDFKVLPQEAEEENR   185
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RESULT 4
US-08-846-762-92
; Sequence 92, Application US/08846762A
; Patent No. 5994072
; GENERAL INFORMATION:
;   Patent No. 5994072
;   APPLICANT: Lam, Joseph S.
;   APPLICANT: Burrows, Lori
;   APPLICANT: Charter, Deborah
;   APPLICANT: de Kievit, Teresa
;   TITLE OF INVENTION: No. 599407ze1 Proteins Involved in the Synthesis and Assembly
;   TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
;   FILE REFERENCE: 6580-089
;   CURRENT APPLICATION NUMBER: US/08/846,762A
;   CURRENT FILING DATE: 1997-04-30
;   NUMBER OF SEQ ID NOS: 100
;   SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 92
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92

Query Match        6.9%;  Score 82.5;  DB 1;  Length 341;
Best Local Similarity   24.0%;  Pred. No. 0.67;
Matches 31;  Conservative 20;  Mismatches 51;  Indels 27;  Gaps 4;

Qy   47  GISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVF   106
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Qy  107  RFKVLILAYAVCRLRHWWAIALTTTAVTSAFLLAKVILSKLFSQGARFGYVLPIISFILAWI   166
Db  283  RFK------------RHLPVTLSAIAINIWLFPIALLAGL----NIVNPIIALIISYI   325

RESULT 5
US-09-489-039A-9711
; Sequence 9711, Application US/0489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;   Patent No. 6610836
;   APPLICANT: Gary Breton et. al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;   TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 2709.2004001
;   CURRENT APPLICATION NUMBER: US/09/489,039A
;   CURRENT FILING DATE: 2000-01-27
;   PRIOR APPLICATION NUMBER: US 60/117,747
;   PRIOR FILING DATE: 1999-01-29
;   NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO: 9711
;   LENGTH: 350

Qy  167  ETWFLDFKV   175
Db  326  PLIYIDYKL   334
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;  TYPE: PRT
;  ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9711

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Best Local Similarity  31.8%;  Pred. No. 1.2;
Matches  21;  Conservative  15;  Mismatches  21;  Indels  9;  Gaps  3;

Qy    111 LILAYAVCRLRHWAIALITAVTSAFLLAKVILSKL------FSQGAFGYVLPIISF---IL 163
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Db     83 LILAVSIPLPAPWWWVLGTAF--AVVIAKQLYGGLGHNPFNPAMIGYVVLLISFPPVQMT 140

Qy    164 AWIETW 169
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Db    141 SWLPSY 146
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RESULT 6
US-10-226-629A-16
Sequence 16, Application US/10226629A
Patent No. 6960431
GENERAL INFORMATION:
  APPLICANT: Myriad Genetics, Inc.
  APPLICANT: Morham, Scott
  APPLICANT: Zavitz, Kenton
  APPLICANT: Hobden, Adrian
  TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
  FILE REFERENCE: 5006.01
  CURRENT APPLICATION NUMBER: US/10/226,629A
  CURRENT FILING DATE: 2002-08-22
  PRIOR APPLICATION NUMBER: US 60/314,182
  PRIOR FILING DATE: 2001-08-22
  NUMBER OF SEQ ID NOS: 736
  SOFTWARE: Patentin version 3.1
  SEQ ID NO 16
  LENGTH: 891
  TYPE: PRT
  ORGANISM: Vaccinia virus
US-10-226-629A-16

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Query Match     6.7%;  Score 80.5;  DB 2;  Length 891;
Best Local Similarity  23.3%;  Pred. No. 4.5;
Matches  38;  Conservative  36;  Mismatches  70;  Indels  19;  Gaps  7;

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Db    717 NMTNITT-DMINASLKNTISKDNNMLVSQALNSVANRSKQKIGDLRQSSCKMALLFKNL 774

Qy     66 VTLLWIELNVNGGIENTLEKEVMQ-YDYY-----SSYFDIFLLAVRFKVLILAYAVCR 119
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Db    775 ATSIYTIERIFNAKVGDDVKASMLEKYKVFFDISMSLYKDLIAMENLKAMLYIIRRSGCR 834

Qy    120 LRHWWAIALATTI--AVTSAFLLAKVILSKL------FSQGAFGYV 155
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Db    835 IDD---AQITTDDLVKSYSLIRPKILSMINYYNEMSRGYFEHM 874
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RESULT 7
US-09-171-699-4
Sequence 4, Application US/0917169
Patent No. 648389
GENERAL INFORMATION:
  APPLICANT: The Wistar Institute of, Anatomy & Biology
  APPLICANT: Gonczol, Eva
  APPLICANT: Berencsi, Klara
  APPLICANT: Kari, Csaba
  TITLE OF INVENTION: No. 648389el Cytomegalovirus DNA Constructs and
         Uses Therefor
  NUMBER OF SEQUENCES: 10
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Howson and Howson
  STREET: Spring House Corporate Center, P.O. Box 457
  CITY: Spring House

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;  STATE: Pennsylvania
;  COUNTRY: USA
;  ZIP: 19477
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/171,699
  FILING DATE: 19-Jan-1999
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/015,717
  FILING DATE: 23-APR-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Kodroff, Cathy A.
  REGISTRATION NUMBER: 33,980
  REFERENCE/DOCKET NUMBER: WST66APCT
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 215-540-9200
  TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 406 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-171-699-4
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Query Match     6.7%;  Score 79.5;  DB 2;  Length 406;
Best Local Similarity  19.3%;  Pred. No. 1.9;
Matches  52;  Conservative  36;  Mismatches  67;  Indels  115;  Gaps  12;

Qy     14 GSQSSHASLRNIHSINPTQLMARIESY-----EGREKKGISDVRRTFCLFVTFDLLFVTL 68
            |:|::|:|:|:|:  |:   | :| |:        |||||||||::|::||:::|:|| ||:
Db    142 GCSQAMAALQNLPQCSPDEIMAYAQKIFKILDEERDK--------VLTHIDHIFMDI 190

Qy     69 LWIIELNVNGGIENTLEKEVMQYDY------YSSYFDIFLLAVRFKVLILAYAVCRL 120
            | |:::| |||| |:|| | || | |      || ||| :|||||:|||||:: |::|
Db    191 L-----TTCVETMCNEYKVTSDACMMTMYGGISLLSEF--------CRV 226

Qy    121 RHWWAIALTTTAVTSAFLLAK-----------VILSKLFSQGAFGYVL----- 156
            | |   |:| |||||||||:|               :||||||||:
Db    227 LSCYVLEETSV-----MLAKRPLIITKPEVISVMKRRIEEICMKVFAQ----YILGADPLR 277

Qy    157 ---PIISFILAWIETWFLDFKVLPQEAEEERRLLIVQDASERAALIPGGLSDGQFYSPPE 213
            :  |:|:||| :|  :|::: |: |:|::| |:  |:  |:::|::|:||:| ||
Db    278 VCSPSVD-----------DLRAIAEESDEEEAIVAYTLATR----------GASSSDSLVSPPE 320

Qy    214 S---------EAGSEAEAEKQDSEK 229
                       |: |:| | :|::|
Db    321 SPVPATIPLSSVIVAENSDQEESEQSDEEE 350
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RESULT 8
PCT-US94-021107-2
Sequence 2, Application PCT/US9402107
GENERAL INFORMATION:
  APPLICANT: The Wistar Institute of, Aviatomy and Biology
  TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
  NUMBER OF SEQUENCES: 4
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Howson and Howson
  STREET: Spring House Corporate Cntr, PO Box 457
  CITY: Spring House
  STATE: Pennsylvania
  COUNTRY: USA
  ZIP: 19477
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US94/02107
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:
;   CLASSIFICATION:
;   FILING DATE:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/017,130
;   FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Bak, Mary E.
;   REGISTRATION NUMBER: 31,215
;   REFERENCE/DOCKET NUMBER: WST6PCT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 215-540-9200
;   TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 406 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
; PCT-US94-02107-2

Query Match      6.7%;  Score 79.5;  DB 4;  Length 406;
Best Local Similarity   19.3%;  Pred. No. 1.9;
Matches  52;  Conservative  36;  Mismatches  67;  Indels 115;  Gaps  12;

Qy     14  GSQSSHASLRNIHSINPTQLMARIESY------EGREKKGISDVRRTFCLFVTFDLLFVTL  68
               :  :||: || ||::::| :  :       |:|| :||: ||::: :| | |||
Db    142  GCSQAMAALQNLPQCSPDEIMAYAQKIFKILDEERDK----------VLTHIDHIFMDI  190

Qy     69  LWIIELNVNGGIENTLEKEVMQYDY------YSSYFDIFLLAVRFKVLILAYAVCRL  120
               ||| :|    ||: |  :|          |:| ||||||  |   || ||| :|
Db    191  L------TTCVETMCNEYKVVTSDACMWTMYGGISLLSEF---------CRV  226

Qy    121  RHWWAIALTTAVTSAFLLAK-----------VILSKLFSQGGAFGYVL------  156
               :|:|  || | | |  |              |:||||||:||| ||
Db    227  LSCVYLEETSV----MLAKRPLITKPEVISVMKRRIEEICMKVPAQ---YILGADPLR  277

Qy    157  ---PIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPE  213
               :||:| :| |:|| | || || ||| :||| ||:| |||||:|||||||||
Db    278  VCSPSVD------------DLRAIAEESDEEAIVAYTLATR-----GASSSDSLVSPPE  320

Qy    214  S--------EAGSEEAEEKQDSEK  229
                        |:|:|::| :|:|
Db    321  SPVPATIPLSSVIVAENSDQEESEQSDEEE  350
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; RESULT 9
; US-09-976-594-503
; Sequence 503, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;   APPLICANT: Furness, Michael
;   APPLICANT: Buchbinder, Jenny
;   TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;   FILE REFERENCE: PA-0041 US
;   CURRENT APPLICATION NUMBER: US/09/976,594
;   CURRENT FILING DATE: 2001-10-12
;   PRIOR APPLICATION NUMBER: 60/240,409
;   PRIOR FILING DATE: 2000-10-12
;   NUMBER OF SEQ ID NOS: 1143
;   SOFTWARE: PERL Program
; SEQ ID NO 503
;   LENGTH: 723
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;     NAME/KEY: misc_feature
;     OTHER INFORMATION: Incyte ID No. 6673549
; US-09-976-594-503
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; RESULT 10
; US-09-270-767-41033
; Sequence 41033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41033
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;     OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-41033

Query Match      6.7%;  Score 79.5;  DB 2;  Length 723;
Best Local Similarity   18.0%;  Pred. No. 4.3;
Matches  34;  Conservative  40;  Mismatches  58;  Indels  57;  Gaps  8;

Qy     58  FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVRFKVLI-----  112
               ||:|:|::  :| : :||:| ||:||| |      |:| ||||||  |:|:
Db     13  FMSVDICVTTAIYVF-------SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLGATIG  67

Qy    113  ----LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ---------------  154
               :|||:|  | | || | |||::| || | |||||
Db     68  VAKNSALGPRRLRASWLVISLVCLFVGIYAMVKLL----LFSEVRRPIRDPMFWALFVWTY  124

Qy    155  VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY-----  209
               ||:|| :| |:|| | ||    | :  | |:||    |     ||:  |||
Db    125  ISLGASFLLWWL---------------------LSTVRPGIQ--ALEPGAATEAEGFPGSGR  163

Qy    210  SPPESEAGS  218
               ||| ::|
Db    164  PPPEQASGA  172
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; RESULT 11
; US-09-270-767-56249
; Sequence 56249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56249
;   LENGTH: 221
;   TYPE: PRT

Query Match      6.6%;  Score 78.5;  DB 2;  Length 221;
Best Local Similarity   22.5%;  Pred. No. 1.1;
Matches  38;  Conservative  33;  Mismatches  73;  Indels  25;  Gaps  7;

Qy     56  CLFVTFDL----LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVRFKVLI  112
               |:| |||:   | :| : :|||:|| ||:||| | |       |||||||:| ||:
Db     17  CIYIYSSMDQFIFIIILILLTCLSFVEXYLFVNILXIDNYIGNXNVFLFFLLLFQXII  76

Qy    113  LAYAVCRLRHWWAIALTT--AVTSAFLLAKVILSKLFSQGGAFGYVL-PIISFILAWIETW  169
               ||| :|:  |  |||:|   |:| ||:| | :: ||    | ||  ||:| :| |:|
Db     77  VVYFCCSFCTTYQLLQGTYNSINFRNLKNLSLT--------LGFIISPPISIHFSYLPHY  129

Qy    170  FLDFKVLPQEAEEENRLL------IVQDASERAAL--IPGGLSDGQF  208
               || |||||   |: ||     |:|||||| | | |||||:|||
Db    130  LVNNSVLHLKNVXIQEFLDXVVKCFFILRASFRFCLKDIPNGL--GQF  176
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;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56249

Query Match             Best Local Similarity  22.5%;  Score 78.5;  DB 2;  Length 221;
Matches  38;  Conservative  33;  Mismatches  73;  Indels  25;  Gaps  7;

Qy   56 CLFVTFDL---LFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI 112
           :  ::    :: ::  : :      :       : : ::     :
Db   17 CIIYSSMDQFLFIIILLILTCLSFVEXYLFVNILXIDNYIGNXNVFLFFLLLFQXII 76

Qy  113 LAYAVCRLRIHWWAIALITT-AVTSAFLLAKVILSKLFSQGAFGYVL-PIISFILAWIETW 169
           :  :        :   :::   :  : :        ::  :  :   :
Db   77 VVYFCCSFCTTYQLIQGTYNSINFRFNLKNLSLT------LGFLISPPISIHFSYLPHY 129

Qy  170 FLDFKVLPQEAEEENRLL----------IVQDASERAAL--IPGGLSDGQF 208
           ::         :      :::         :  :::
Db  130 LVNNSVLHLKNVXIQEFLDXVVKCFFFILRASFRFCLKDIPNGL--GQF 176


RESULT 12
US-09-724-653-2
;   Sequence 2, Application US/0972465
;   Patent No. 6830913
;   GENERAL INFORMATION:
;   APPLICANT: Ling, Victor
;   TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
;   FILE REFERENCE: APZ-004CP
;   CURRENT APPLICATION NUMBER: US/09/724,653
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: 60/167,930
;   PRIOR FILING DATE: 1999-11-29
;   NUMBER OF SEQ ID NOS: 20
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 2
;   LENGTH: 766
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-653-2

Query Match             Best Local Similarity  18.0%;  Score 78.5;  DB 2;  Length 766;
Matches  34;  Conservative  39;  Mismatches  59;  Indels  57;  Gaps  8;

Qy   58 FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
          :|::|:|:  :||::  :   ::    :  : ::    : ::  ::|:  :: :|:
Db   13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLGATIG 67

Qy  113 ---LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ----------GAFGY 154
            |||  : :  ||::| ::  ::  :||::||||  ::|||||  :|
Db   68 VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFWTY 124

Qy  155 VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
          :|:: |||   |  |::  |:  :|||:|||: :|:  :||  : ||:||:::|
Db  125 ISLGASFLLWWL--------------------LSTVRPGTQ-ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
          .||| :|:
Db  164 PPPEQASGA 172


RESULT 13
US-09-724-653-14
;   Sequence 14, Application US/0972465
;   Patent No. 6830913
;   GENERAL INFORMATION:
;   APPLICANT: Ling, Victor
;   TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
;   FILE REFERENCE: APZ-004CP
;   CURRENT APPLICATION NUMBER: US/09/724,653
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: 60/167,930
;   PRIOR FILING DATE: 1999-11-29
;   NUMBER OF SEQ ID NOS: 20
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 14
;   LENGTH: 766
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-653-14

Query Match             Best Local Similarity  18.0%;  Score 78.5;  DB 2;  Length 766;
Matches  34;  Conservative  39;  Mismatches  59;  Indels  57;  Gaps  8;

Qy   58 FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
          :|::|:|:  :||::  :   ::    :  : ::    : ::  ::|:  :: :|:
Db   13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLGATIG 67

Qy  113 ---LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ----------GAFGY 154
            |||  : :  ||::| ::  ::  :||::||||  ::|||||  :|
Db   68 VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFWTY 124

Qy  155 VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
          :|:: |||   |  |::  |:  :|||:|||: :|:  :||  : ||:||:::|
Db  125 ISLGASFLLWWL--------------------LSTVRPGTQ-ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
          .||| :|:
Db  164 PPPEQASGA 172


RESULT 14
US-09-724-653-15
;   Sequence 15, Application US/0972465
;   Patent No. 6830913
;   GENERAL INFORMATION:
;   APPLICANT: Ling, Victor
;   TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
;   FILE REFERENCE: APZ-004CP
;   CURRENT APPLICATION NUMBER: US/09/724,653
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: 60/167,930
;   PRIOR FILING DATE: 1999-11-29
;   NUMBER OF SEQ ID NOS: 20
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 15
;   LENGTH: 766
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-653-15

Query Match             Best Local Similarity  18.0%;  Score 78.5;  DB 2;  Length 766;
Matches  34;  Conservative  39;  Mismatches  59;  Indels  57;  Gaps  8;

Qy   58 FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
          :|::|:|:  :||::  :   ::    :  : ::    : ::  ::|:  :: :|:
Db   13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLGATIG 67

Qy  113 ---LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ----------GAFGY 154
            |||  : :  ||::| ::  ::  :||::||||  ::|||||  :|
Db   68 VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFWTY 124

Qy  155 VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
          :|:: |||   |  |::  |:  :|||:|||: :|:  :||  : ||:||:::|
Db  125 ISLGASFLLWWL--------------------LSTVRPGTQ-ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
          .||| :|:
Db  164 PPPEQASGA 172


RESULT 15
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US-09-248-796A-20444
; Sequence 20444, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;   APPLICANT: Keith Weinstock et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;   TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.132
;   CURRENT APPLICATION NUMBER: US/09/248,796A
;   CURRENT FILING DATE: 1999-02-12
;   PRIOR APPLICATION NUMBER: US 60/074,725
;   PRIOR FILING DATE: 1998-02-13
;   PRIOR APPLICATION NUMBER: US 60/096,409
;   PRIOR FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 28208
;   SEQ ID NO 20444
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-20444

Query Match   6.5%; Score 78; DB 2; Length 228;
Best Local Similarity   22.1%; Pred. No 1.3;
Matches 32; Conservative 32; Mismatches 49; Indels 32; Gaps 7;

Qy   63 LLFVTL------LWIIELNVN---GGIENTLEKEVMQYDYYSSYF----------DIFLLAVF 106
           :|:| ||:| ||:|
Db   91 LVFTALTSYGAFWLSFPAINIPTFGILAAYQKDMTQLSSALAFYLIIAWAILSFIFMLLTF 150

Qy   107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF----- 161
           : |||: :|::| |||:   ::| :: |: : :
Db   151 KSTVLLSGFFLC------LTALFSLLSASYFVGGSVALTK--AAGAFGVIAVVAALYDTFA 202

Qy   162 ILAWIETWFLDFKVLP---QEAEEE 183
           :|:| |:|
Db   203 LLATKQNSYFTLPVIPLPGGSEAKQE 227

Search completed: May 12, 2006, 20:48:56
Job time : 61 secs

OM protein - protein search, using sw model

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                     GenCore version 5.1.8
                     Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:              May 12, 2006, 21:12:04 ; Search time 66 Seconds
                                               (without alignments!)
                                               1481.395 Million cell updates/sec

Perfect score:       1195
Sequence:            1 MNHLPEDMENALTGSQSSHA..........EAGSEEAEEKQDSEKPLLEL 234

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                     Gapop 10.0 , Gapext 0.5

Searched:            1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:   1867569

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Maximum DB seq length: 200000000

Post-processing:     Minimum Match 0%
                     Maximum Match 100%
                     Listing first 1500 summaries

Database :           Published Applications AA Main:*
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                     2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                     3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                     4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                     5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                     6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
449	1195	100.0	234	4	US-10-223-085-62	Sequence 62, Appl
466	1195	100.0	234	4	US-10-223-084-62	Sequence 62, Appl
467	1195	100.0	234	4	US-10-223-088-62	Sequence 62, Appl
468	1195	100.0	234	4	US-10-223-090-62	Sequence 62, Appl
470	1195	100.0	234	4	US-10-223-087-62	Sequence 62, Appl
478	1195	100.0	234	4	US-10-223-086-62	Sequence 62, Appl
481	1195	100.0	234	4	US-10-223-089-62	Sequence 62, Appl
498	1195	100.0	234	4	US-10-174-587-66	Sequence 66, Appl
562	1195	100.0	234	4	US-10-223-081-62	Sequence 14, Appl
640	1195	100.0	234	4	US-10-063-742-14	Sequence 14, Appl
650	1195	100.0	234	4	US-10-223-082-62	Sequence 62, Appl
665	1195	100.0	234	4	US-10-144-194A-20	Sequence 20, Appl
670	1195	100.0	234	4	US-10-305-654-62	Sequence 62, Appl
675	1195	100.0	234	5	US-10-491-056-62	Sequence 20, Appl
681	1195	100.0	234	4	US-10-972-317-14	Sequence 14, Appl
682	1195	100.0	234	5	US-10-491-566-20	Sequence 20, Appl
683	1195	100.0	234	4	US-10-485-555-36	Sequence 36, Appl
687	1188	99.4	234	4	US-10-262-839-84	Sequence 84, Appl
688	1024	85.7	201	4	US-10-264-237-2663	Sequence 2663, Ap
689	985	82.4	198	4	US-10-262-839-82	Sequence 82, Appl
690	669.5	56.0	176	4	US-10-104-047-2567	Sequence 2567, App
691	664	55.6	445	4	US-10-177-293-296	Sequence 296, App
692	664	55.6	445	5	US-10-435-696-33	Sequence 33, Appl
693	625	52.3	534	5	US-10-450-763-35857	Sequence 35857, A
694	578	48.4	412	5	US-11-097-213-22	Sequence 22, Appl
695	343	28.7	580	6	US-11-097-143-6696	Sequence 6696, Ap
696	91	7.6	373	4	US-10-091-007-198	Sequence 198, App
697	90.5	7.6	803	4	US-10-437-963-136814	Sequence 136814,
698	87.5	7.3	516	3	US-09-925-298-653	Sequence 653, App
699	87	7.3	516	5	US-10-102-806-653	Sequence 653, App
700	87	7.3	421	5	US-10-741-600-929	Sequence 929, App
701	85.5	7.3	223	5	US-10-741-600-926	Sequence 926, App
702	85.5	7.2	285	5	US-10-741-600-921	Sequence 921, App
703	85.5	7.2	315	5	US-10-741-600-925	Sequence 925, App
704	85.5	7.2	323	5	US-10-741-600-923	Sequence 923, App
705	85.5	7.2	323	5	US-10-741-600-924	Sequence 924, App
706	85.5	7.2	338	5	US-10-741-600-928	Sequence 928, App
707	85.5	7.2	339	5	US-10-741-600-930	Sequence 930, App
708	85.5	7.2	339	5	US-10-741-600-932	Sequence 932, App
709	85.5	7.2	390	5	US-10-741-600-927	Sequence 927, App
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813	75.5	6.3	352	4	US-10-771-241-293	Sequence 293, App
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1480	68	5.7	488	4	US-10-755-889-170	Sequence 170, Appl
1481	68	5.7	488	4	US-10-925-095-561	Sequence 561, Appl
1482	68	5.7	490	3	US-10-925-095-18	Sequence 18, Appl
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1484	68	5.7	490	4	US-10-243-351-2	Sequence 2, Appli
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1486	68	5.7	542	4	US-10-450-763-56651	Sequence 56651,
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1489	68	5.7	562	4	US-10-275-026A-5907	Sequence 5907, App
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1494	68	5.7	714	4	US-10-090-455-13	Sequence 13, Appl
1495	68	5.7	727	3	US-10-443-963-195183	Sequence 195183,
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1498	68	5.7	799	4	US-10-757-774-2313	Sequence 2313, Ap
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| 88 | 71 | 5.9 | 646 | 11 | US-11-096-568A-27468 | Sequence 27468, A |
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| 105 | 70 | 5.9 | 367 | 11 | US-11-096-568A-22840 | Sequence 2840, A |
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| 108 | 70 | 5.9 | 475 | 11 | US-11-096-568A-4755 | Sequence 4755, Ap |
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| 110 | 70 | 5.9 | 494 | 11 | US-11-087-099-10612 | Sequence 10612, A |
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| 157 | 68.5 | 5.7 | 963 | 11 | US-11-188-298-4720 | Sequence 4720, Ap |
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| 159 | 68 | 5.7 | 247 | 9 | US-11-703-799B-152 | Sequence 152, App |
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| 204 | 66 | 5.6 | 447 | 11 | US-11-232-805-7 | Sequence 7, Appli |
| 205 | 66 | 5.6 | 450 | 11 | US-10-784-004-364 | Sequence 364, App |
| 206 | 66 | 5.6 | 461 | 11 | US-10-784-004-926 | Sequence 926, App |
| 207 | 66 | 5.5 | 461 | 9 | US-11-087-099-7597 | Sequence 7597, App |
| 208 | 66 | 5.5 | 573 | 11 | US-11-087-099-6963 | Sequence 6963, App |
| 209 | 66 | 5.5 | 573 | 11 | US-11-045-004-1518 | Sequence 1518, Ap |
| 210 | 66 | 5.5 | 582 | 11 | US-11-096-568A-28534 | Sequence 28534, A |
| 211 | 66 | 5.5 | 693 | 11 | US-11-096-568A-28533 | Sequence 28533, A |
| 212 | 66 | 5.5 | 705 | 11 | US-11-096-568A-28532 | Sequence 28532, A |
| 213 | 66 | 5.5 | 749 | 11 | US-11-079-463-5493 | Sequence 5493, Ap |
| 214 | 66 | 5.5 | 915 | 11 | US-11-156-084-119 | Sequence 119, App |
| 215 | 66 | 5.5 | 1106 | 11 | US-11-188-298-21803 | Sequence 21803, A |
| 216 | 66 | 5.5 | 1250 | 9 | US-10-531-036-37 | Sequence 37, Appl |
| 217 | 65.5 | 5.5 | 304 | 11 | US-11-188-298-21577 | Sequence 21577, A |
| 218 | 65.5 | 5.5 | 356 | 11 | US-11-188-298-15178 | Sequence 15178, A |
| 219 | 65.5 | 5.5 | 379 | 11 | US-11-079-463-7981 | Sequence 7981, Ap |
| 220 | 65.5 | 5.5 | 382 | 11 | US-11-146-428-72 | Sequence 72, Appl |
| 221 | 65.5 | 5.5 | 383 | 11 | US-11-188-298-6963 | Sequence 6963, App |
| 222 | 65.5 | 5.5 | 444 | 8 | US-11-188-298-21651 | Sequence 21651, A |
| 223 | 65.5 | 5.5 | 491 | 11 | US-10-511-937-3003 | Sequence 3003, Ap |
| 224 | 65.5 | 5.5 | 491 | 11 | US-11-045-004-1074 | Sequence 1074, Ap |
| 225 | 65.5 | 5.5 | 575 | 11 | US-11-045-004-1461 | Sequence 1461, Ap |
| 226 | 65.5 | 5.5 | 583 | 11 | US-11-045-004-422 | Sequence 422, App |
| 227 | 65.5 | 5.5 | 617 | 11 | US-11-264-996-1671 | Sequence 1671, Ap |
| 228 | 65.5 | 5.5 | 618 | 11 | US-11-045-004-200 | Sequence 200, App |
| 229 | 65.5 | 5.5 | 721 | 11 | US-11-045-004-354 | Sequence 354, App |
| 230 | 65.5 | 5.5 | 902 | 11 | US-11-045-004-660 | Sequence 660, App |
| 231 | 65.5 | 5.5 | 1143 | 11 | US-11-188-298-12745 | Sequence 12745, A |
| 232 | 65.5 | 5.5 | 2420 | 11 | US-11-072-512-2802 | Sequence 2802, Ap |
| 233 | 65 | 5.4 | 159 | 11 | US-11-087-099-9017 | Sequence 9017, App |
| 234 | 65 | 5.4 | 176 | 11 | US-11-087-099-7545 | Sequence 7545, Ap |
| 235 | 65 | 5.4 | 176 | 9 | US-11-165-697-46 | Sequence 46, Appl |
| 236 | 65 | 5.4 | 180 | 11 | US-11-165-697-45 | Sequence 45, Appl |
| 237 | 65 | 5.4 | 250 | 11 | US-10-098-686-11014 | Sequence 11014, A |
| 238 | 65 | 5.4 | 344 | 11 | US-11-199-821-6 | Sequence 6, Appli |
| 239 | 65 | 5.4 | 415 | 11 | US-10-793-626-780 | Sequence 780, App |
| 240 | 65 | 5.4 | 432 | 9 | US-10-784-004-685 | Sequence 685, Ap |
| 241 | 65 | 5.4 | 461 | 9 | US-10-784-004-1071 | Sequence 1071, Ap |
| 242 | 65 | 5.4 | 461 | 11 | US-10-467-657-3124 | Sequence 3124, Ap |
| 243 | 65 | 5.4 | 481 | 11 | US-10-467-657-4866 | Sequence 4866, Ap |
| 244 | 65 | 5.4 | 600 | 9 | US-11-096-568A-26497 | Sequence 26497, A |
| 245 | 65 | 5.4 | 718 | 9 | US-11-079-463-7103 | Sequence 7103, A |
| 246 | 65 | 5.4 | 1220 | 11 | US-11-096-568A-29542 | Sequence 29542, A |
| 247 | 64.5 | 5.4 | 213 | 11 | | Sequence 29542, A |

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| 248 | 64.5 | 5.4 | 218 | 11 | US-11-096-568A-7345 | Sequence 7346, Ap |
| 249 | 64.5 | 5.4 | 308 | 11 | US-11-096-568A-7345 | Sequence 7345, Ap |
| 250 | 64.5 | 5.4 | 311 | 11 | US-11-188-298-10501 | Sequence 10501, A |
| 251 | 64.5 | 5.4 | 314 | 11 | US-11-055-822-284 | Sequence 284, App |
| 252 | 64.5 | 5.4 | 324 | 11 | US-11-079-463-6638 | Sequence 6638, Ap |
| 253 | 64.5 | 5.4 | 400 | 9 | US-10-499-210-2 | Sequence 2, Appli |
| 254 | 64.5 | 5.4 | 416 | 11 | US-11-045-004-473 | Sequence 473, App |
| 255 | 64.5 | 5.4 | 450 | 11 | US-10-507-720-18 | Sequence 18, Appl |
| 256 | 64.5 | 5.4 | 486 | 11 | US-10-507-720-10 | Sequence 10, Appl |
| 257 | 64.5 | 5.4 | 495 | 9 | US-11-210-316-10 | Sequence 20, Appl |
| 258 | 64.5 | 5.4 | 567 | 11 | US-10-508-263-20 | Sequence 7, Appli |
| 259 | 64.5 | 5.4 | 622 | 11 | US-11-120-422-7 | Sequence 780, App |
| 260 | 64.5 | 5.4 | 629 | 11 | US-11-045-004-780 | Sequence 24, Appl |
| 261 | 64.5 | 5.4 | 693 | 11 | US-11-232-406A-24 | Sequence 11111, A |
| 262 | 64.5 | 5.4 | 747 | 11 | US-11-098-686-11111 | Sequence 2, Appli |
| 263 | 64.5 | 5.4 | 847 | 11 | US-11-210-316-2 | Sequence 1706, Ap |
| 264 | 64.5 | 5.4 | 1771 | 9 | US-11-087-099-1706 | Sequence 1532, Ap |
| 265 | 64.5 | 5.4 | 219 | 11 | US-11-098-686-1532 | Sequence 10094, A |
| 266 | 64 | 5.4 | 235 | 11 | US-10-506-454-10094 | Sequence 3045, Ap |
| 267 | 64 | 5.4 | 239 | 9 | US-10-895-064-1311 | Sequence 1311, Ap |
| 268 | 64 | 5.4 | 244 | 11 | US-11-129-741-1311 | Sequence 1135, Ap |
| 269 | 64 | 5.4 | 331 | 11 | US-11-087-099-1135 | Sequence 979, App |
| 270 | 64 | 5.4 | 402 | 11 | US-11-172-740-979 | Sequence 1429, Ap |
| 271 | 64 | 5.4 | 422 | 11 | US-11-045-004-1429 | Sequence 9711, Ap |
| 272 | 64 | 5.4 | 422 | 11 | US-11-087-099-9711 | Sequence 20014, A |
| 273 | 64 | 5.4 | 439 | 11 | US-11-188-298-20014 | Sequence 32641, A |
| 274 | 64 | 5.4 | 457 | 11 | US-11-096-568A-32641 | Sequence 2903, Ap |
| 275 | 64 | 5.4 | 463 | 11 | US-11-087-099-2903 | Sequence 2755, Ap |
| 276 | 64 | 5.4 | 477 | 11 | US-11-087-099-2755 | Sequence 1186, Ap |
| 277 | 64 | 5.4 | 479 | 11 | US-11-098-686-1186 | Sequence 10838, A |
| 278 | 64 | 5.4 | 480 | 11 | US-11-087-099-10838 | Sequence 33998, A |
| 279 | 64 | 5.4 | 499 | 11 | US-11-096-568A-33998 | Sequence 2096, Ap |
| 280 | 64 | 5.4 | 506 | 9 | US-11-467-657-2096 | Sequence 32640, A |
| 281 | 64 | 5.4 | 512 | 11 | US-11-096-568A-32640 | Sequence 7971, Ap |
| 282 | 64 | 5.4 | 534 | 11 | US-11-188-298-7971 | Sequence 920, App |
| 283 | 64 | 5.4 | 535 | 11 | US-10-793-626-920 | Sequence 32639, A |
| 284 | 64 | 5.4 | 557 | 11 | US-11-096-568A-32639 | Sequence 10483, A |
| 285 | 64 | 5.4 | 557 | 11 | US-11-098-686-10483 | Sequence 33997, A |
| 286 | 64 | 5.4 | 582 | 9 | US-11-096-568A-33997 | Sequence 558, App |
| 287 | 64 | 5.4 | 589 | 11 | US-10-330-773-558 | Sequence 9982, Ap |
| 288 | 64 | 5.4 | 632 | 11 | US-11-188-298-9982 | Sequence 33996, A |
| 289 | 64 | 5.4 | 674 | 11 | US-11-096-568A-33996 | Sequence 14572, A |
| 290 | 64 | 5.4 | 678 | 9 | US-11-188-298-14572 | Sequence 7198, App |
| 291 | 64 | 5.4 | 849 | 11 | US-11-188-298-7198 | Sequence 8045, Ap |
| 292 | 64 | 5.4 | 875 | 11 | US-11-188-298-8045 | Sequence 2555, Ap |
| 293 | 64 | 5.4 | 896 | 11 | US-11-045-004-2555 | Sequence 30497, A |
| 294 | 64 | 5.4 | 911 | 11 | US-11-096-568A-30497 | Sequence 27, Appl |
| 295 | 64 | 5.4 | 911 | 11 | US-11-096-568A-27 | Sequence 1019, Ap |
| 296 | 64 | 5.4 | 991 | 11 | US-11-188-298-1019 | Sequence 277, Appl |
| 297 | 64 | 5.4 | 1462 | 9 | US-10-501-035-277 | Sequence 6295, Ap |
| 298 | 63.5 | 5.4 | 313 | 11 | US-11-096-568A-6295 | Sequence 6294, Ap |
| 299 | 63.5 | 5.4 | 334 | 11 | US-11-096-568A-6294 | Sequence 351, Appl |
| 300 | 63.5 | 5.4 | 337 | 11 | US-11-222-874-2 | Sequence 2, Appli |
| 301 | 63.5 | 5.4 | 380 | 11 | US-10-784-004-351 | Sequence 921, App |
| 302 | 63.5 | 5.3 | 380 | 9 | US-10-784-004-921 | Sequence 29262, A |
| 303 | 63.5 | 5.3 | 438 | 11 | US-11-096-568A-29262 | Sequence 28704, A |
| 304 | 63.5 | 5.3 | 450 | 11 | US-11-096-568A-28704 | Sequence 10325, A |
| 310 | 63.5 | 5.3 | 509 | 11 | US-11-096-568A-10325 | Sequence 29261, A |
| 311 | 63.5 | 5.3 | 511 | 11 | US-11-096-568A-29261 | Sequence 10, Appl |
| 312 | 63.5 | 5.3 | 555 | 11 | US-11-226-480-10 | Sequence 471, App |
| 313 | 63.5 | 5.3 | 568 | 11 | US-11-000-463-471 | Sequence 674, App |
| 314 | 63.5 | 5.3 | 568 | 11 | US-11-228-079-10 | Sequence 568, App |
| 315 | 63.5 | 5.3 | 577 | 11 | US-11-264-096-1782 | Sequence 1782, Ap |
| 316 | 63.5 | 5.3 | 590 | 11 | US-11-079-463-8330 | Sequence 8330, Ap |
| 317 | 63.5 | 5.3 | 632 | 11 | US-11-188-298-3895 | Sequence 3895, Ap |
| 318 | 63.5 | 5.3 | 668 | 11 | US-11-098-686-11201 | Sequence 11201, A |
| 319 | 63.5 | 5.3 | 674 | 11 | US-11-000-463-471 | Sequence 279, App |
| 320 | 63.5 | 5.3 | 679 | 9 | US-10-506-454-279 | Sequence 321, App |
| 321 | 63.5 | 5.3 | 685 | 11 | US-11-506-454-321 | Sequence 5510, Ap |
| 322 | 63.5 | 5.3 | 768 | 11 | US-11-079-463-5510 | Sequence 656, App |
| 323 | 63.5 | 5.3 | 775 | 9 | US-11-453-372-656 | Sequence 2446, Ap |
| 324 | 63.5 | 5.3 | 979 | 11 | US-11-072-512-2446 | Sequence 810, App |
| 325 | 63.5 | 5.3 | 1208 | 9 | US-10-330-773-810 | |

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| 326 | 63.5 | 5.3 | 2080 | 9 | US-10-821-234-1640 | Sequence 1640, Ap |
| 327 | 63.5 | 5.3 | 52 | 7 | US-09-978-360A-557 | Sequence 557, App |
| 328 | 63 | 5.3 | 172 | 11 | US-11-079-463-6028 | Sequence 6028, Ap |
| 329 | 63 | 5.3 | 178 | 9 | US-10-507-355-5 | Sequence 5, Appli |
| 330 | 63 | 5.3 | 178 | 9 | US-10-507-355-6 | Sequence 6, Appli |
| 331 | 63 | 5.3 | 178 | 11 | US-11-087-099-1791 | Sequence 1791, Ap |
| 332 | 63 | 5.3 | 178 | 11 | US-11-087-099-11170 | Sequence 11170, A |
| 333 | 63 | 5.3 | 259 | 9 | US-10-055-877-225 | Sequence 225, App |
| 334 | 63 | 5.3 | 259 | 9 | US-10-055-877-237 | Sequence 237, App |
| 335 | 63 | 5.3 | 259 | 11 | US-11-206-587-27 | Sequence 27, Appl |
| 336 | 63 | 5.3 | 273 | 11 | US-11-206-587-34 | Sequence 34, Appl |
| 337 | 63 | 5.3 | 290 | 11 | US-11-188-298-348 | Sequence 348, Appl |
| 338 | 63 | 5.3 | 332 | 11 | US-11-096-568A-28678 | Sequence 28678, A |
| 339 | 63 | 5.3 | 339 | 11 | US-11-096-568A-31012 | Sequence 31012, A |
| 340 | 63 | 5.3 | 351 | 11 | US-11-096-568A-976 | Sequence 976, App |
| 341 | 63 | 5.3 | 351 | 11 | US-11-087-099-4495 | Sequence 4495, Ap |
| 342 | 63 | 5.3 | 359 | 11 | US-11-096-568A-28677 | Sequence 28677, A |
| 343 | 63 | 5.3 | 359 | 11 | US-11-096-568A-31011 | Sequence 31011, A |
| 344 | 63 | 5.3 | 388 | 11 | US-11-096-568A-14752 | Sequence 14752, A |
| 345 | 63 | 5.3 | 391 | 11 | US-11-096-568A-15310 | Sequence 15310, A |
| 346 | 63 | 5.3 | 410 | 11 | US-11-199-821-7 | Sequence 7, Appli |
| 347 | 63 | 5.3 | 415 | 11 | US-11-096-568A-31010 | Sequence 31010, A |
| 348 | 63 | 5.3 | 422 | 11 | US-11-188-298-13929 | Sequence 13929, A |
| 349 | 63 | 5.3 | 432 | 11 | US-11-096-568A-27614 | Sequence 27614, A |
| 350 | 63 | 5.3 | 446 | 11 | US-11-096-568A-15309 | Sequence 15309, A |
| 351 | 63 | 5.3 | 446 | 11 | US-11-188-298-16813 | Sequence 16813, A |
| 352 | 63 | 5.3 | 449 | 11 | US-11-232-805-27 | Sequence 27, Appl |
| 353 | 63 | 5.3 | 449 | 11 | US-11-096-568A-28676 | Sequence 28676, A |
| 354 | 63 | 5.3 | 450 | 11 | US-11-232-805-26 | Sequence 26, Appl |
| 355 | 63 | 5.3 | 450 | 11 | US-11-096-568A-27613 | Sequence 27613, A |
| 356 | 63 | 5.3 | 450 | 11 | US-11-188-298-20527 | Sequence 20527, A |
| 357 | 63 | 5.3 | 462 | 11 | US-11-096-568A-26653 | Sequence 26653, A |
| 358 | 63 | 5.3 | 496 | 11 | US-11-079-463-9528 | Sequence 9528, Ap |
| 359 | 63 | 5.3 | 509 | 11 | US-11-055-309A-112 | Sequence 112, Appl |
| 360 | 63 | 5.3 | 509 | 11 | US-11-072-175-219 | Sequence 219, App |
| 361 | 62.5 | 5.3 | 532 | 9 | US-10-821-234-918 | Sequence 918, App |
| 362 | 62.5 | 5.3 | 532 | 11 | US-11-096-568A-27612 | Sequence 27612, A |
| 363 | 63 | 5.3 | 533 | 9 | US-11-096-568A-29 | Sequence 29, Appl |
| 364 | 63 | 5.3 | 533 | 11 | US-11-096-568A-10295 | Sequence 10295, A |
| 365 | 63 | 5.3 | 729 | 11 | US-10-793-626-774 | Sequence 774, App |
| 366 | 63 | 5.3 | 1075 | 9 | US-11-098-686-10295 | Sequence 10295, A |
| 367 | 63 | 5.3 | 214 | 9 | US-11-096-568A-20087 | Sequence 20087, A |
| 368 | 63 | 5.3 | 226 | 11 | US-11-096-568A-20887 | Sequence 20887, A |
| 369 | 62.5 | 5.3 | 297 | 11 | US-11-096-568A-6199 | Sequence 6199, Ap |
| 370 | 62.5 | 5.3 | 307 | 11 | US-11-087-099-11577 | Sequence 11577, A |
| 371 | 62.5 | 5.3 | 324 | 11 | US-11-096-568A-20886 | Sequence 20886, A |
| 372 | 62.5 | 5.3 | 353 | 11 | US-11-096-568A-20885 | Sequence 20885, A |
| 373 | 62.5 | 5.3 | 356 | 11 | US-11-188-298-11213 | Sequence 11213, A |
| 374 | 62.5 | 5.2 | 371 | 11 | US-11-096-568A-26653 | Sequence 26653, A |
| 375 | 62.5 | 5.2 | 371 | 11 | US-11-096-568A-20886 | Sequence 20886, A |
| 376 | 62.5 | 5.2 | 371 | 11 | US-11-096-568A-20885 | Sequence 20885, A |
| 377 | 62.5 | 5.2 | 376 | 11 | US-11-096-568A-2555 | Sequence 2555, Ap |
| 378 | 62.5 | 5.2 | 413 | 11 | US-11-188-298-11213 | Sequence 11213, A |
| 379 | 62.5 | 5.2 | 439 | 11 | US-11-096-568A-26653 | Sequence 26653, A |
| 380 | 62.5 | 5.2 | 448 | 11 | US-11-096-568A-6197 | Sequence 6197, Ap |
| 381 | 62.5 | 5.2 | 452 | 11 | US-11-188-298-13966 | Sequence 13966, A |
| 382 | 62.5 | 5.2 | 462 | 11 | US-11-188-298-21326 | Sequence 21326, A |
| 383 | 62.5 | 5.2 | 376 | 11 | US-11-188-298-9945 | Sequence 9945, Ap |
| 384 | 62.5 | 5.2 | 413 | 11 | US-11-045-004-2430 | Sequence 2430, Ap |
| 385 | 62.5 | 5.2 | 439 | 9 | US-11-096-568A-6198 | Sequence 6198, Ap |
| 386 | 62.5 | 5.2 | 448 | 11 | US-11-100-640-34 | Sequence 34, Appl |
| 387 | 62.5 | 5.2 | 452 | 11 | US-11-096-568A-16342 | Sequence 16342, A |
| 388 | 62.5 | 5.2 | 462 | 9 | US-11-087-099-11901 | Sequence 11901, A |
| 389 | 62.5 | 5.2 | 462 | 11 | US-11-087-099-10987 | Sequence 10987, A |
| 390 | 62.5 | 5.2 | 462 | 11 | US-11-096-568A-16342 | Sequence 16342, A |
| 391 | 62.5 | 5.2 | 462 | 11 | US-11-096-568A-12101 | Sequence 12101, A |
| 392 | 62.5 | 5.2 | 470 | 11 | US-11-087-099-10492 | Sequence 10492, A |
| 393 | 62.5 | 5.2 | 470 | 11 | US-11-264-096-1782 | Sequence 1782, Ap |
| 394 | 62.5 | 5.2 | 479 | 11 | US-11-087-099-10492 | Sequence 10492, A |
| 395 | 62.5 | 5.2 | 479 | 11 | US-11-188-298-3895 | Sequence 3895, Ap |
| 396 | 62.5 | 5.2 | 479 | 9 | US-11-873-528-60 | Sequence 60, Appl |
| 397 | 62.5 | 5.2 | 533 | 11 | US-11-096-568A-30130 | Sequence 30130, A |
| 398 | 62.5 | 5.2 | 559 | 11 | US-11-096-568A-4552 | Sequence 4552, Ap |
| 399 | 62.5 | 5.2 | 595 | 11 | US-11-096-568A-9991 | Sequence 9991, Ap |
| 400 | 62.5 | 5.2 | 609 | 11 | US-11-087-099-10492 | Sequence 10492, Ap |
| 401 | 62.5 | 5.2 | 668 | 11 | US-11-052-554A-298 | Sequence 9712, Ap |
| 402 | 62.5 | 5.2 | 696 | 11 | US-11-188-298-20527 | Sequence 20527, A |
| 403 | 62.5 | 5.2 | 863 | 9 | US-10-330-773-849 | Sequence 849, App |

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| 404 | 62.5 | 5.2 | 959  | 11 | US-11-188-298-12621  | Sequence 12621, A |
| 405 | 62.5 | 5.2 | 1144 | 9  | US-10-467-657-1820   | Sequence 1820, A |
| 406 | 62.5 | 5.2 | 3375 | 11 | US-10-044-111-23     | Sequence 23, Appl |
| 407 | 62   | 5.2 | 177  | 11 | US-11-087-099-11875  | Sequence 11875, A |
| 408 | 62   | 5.2 | 178  | 11 | US-11-096-568A-18452 | Sequence 18452, A |
| 409 | 62   | 5.2 | 188  | 11 | US-11-096-568A-18451 | Sequence 18451, A |
| 410 | 62   | 5.2 | 244  | 11 | US-11-087-099-1059   | Sequence 1059, Ap |
| 411 | 62   | 5.2 | 247  | 11 | US-11-045-004-1955   | Sequence 1955, Ap |
| 412 | 62   | 5.2 | 272  | 10 | US-11-024-544A-120   | Sequence 120, Appl |
| 413 | 62   | 5.2 | 272  | 10 | US-11-024-545-48     | Sequence 48, Appl |
| 414 | 62   | 5.2 | 272  | 10 | US-11-185-301-36     | Sequence 36, Appl |
| 415 | 62   | 5.2 | 272  | 10 | US-11-190-750-103    | Sequence 103, Appl |
| 416 | 62   | 5.2 | 272  | 10 | US-11-251-466-22     | Sequence 22, Appl |
| 417 | 62   | 5.2 | 272  | 10 | US-11-254-173-36     | Sequence 36, Appl |
| 418 | 62   | 5.2 | 272  | 11 | US-11-264-784-21     | Sequence 21, Appl |
| 419 | 62   | 5.2 | 272  | 11 | US-11-146-428-58     | Sequence 58, Appl |
| 420 | 62   | 5.2 | 272  | 11 | US-11-225-354-29     | Sequence 29, Appl |
| 421 | 62   | 5.2 | 313  | 11 | US-11-087-099-1059   | Sequence 1059, App |
| 422 | 62   | 5.2 | 313  | 11 | US-10-055-877-234    | Sequence 234, App |
| 423 | 62   | 5.7 | 313  | 11 | US-11-096-568A-18450 | Sequence 18450, Ap |
| 424 | 62   | 5.2 | 353  | 11 | US-11-017-058-9      | Sequence 9, Appli |
| 425 | 62   | 5.2 | 360  | 10 | US-11-242-111-19     | Sequence 19, Appl |
| 426 | 62   | 5.2 | 373  | 11 | US-11-087-099-11566  | Sequence 11566, A |
| 427 | 62   | 5.2 | 379  | 11 | US-11-087-099-12062  | Sequence 12062, A |
| 428 | 62   | 5.2 | 381  | 9  | US-10-793-626-184    | Sequence 184, App |
| 429 | 62   | 5.2 | 394  | 11 | US-11-096-568A-32558 | Sequence 32558, A |
| 430 | 62   | 5.2 | 403  | 11 | US-11-087-099-10953  | Sequence 10953, A |
| 431 | 62   | 5.2 | 417  | 9  | US-10-793-626-950    | Sequence 950, App |
| 432 | 62   | 5.2 | 432  | 11 | US-11-055-822-1096   | Sequence 1096, App |
| 433 | 62   | 5.2 | 435  | 11 | US-11-096-568A-32557 | Sequence 32557, A |
| 434 | 62   | 5.2 | 447  | 11 | US-11-096-568A-32556 | Sequence 32556, A |
| 435 | 62   | 5.2 | 456  | 9  | US-10-467-657-4150   | Sequence 4150, Ap |
| 436 | 62   | 5.2 | 467  | 11 | US-11-188-298-6866   | Sequence 6866, Ap |
| 437 | 62   | 5.2 | 491  | 9  | US-10-511-538-48     | Sequence 48, Appl |
| 438 | 62   | 5.2 | 514  | 11 | US-11-188-298-14827  | Sequence 14827, A |
| 439 | 62   | 5.2 | 516  | 11 | US-11-079-463-6808   | Sequence 6808, Ap |
| 440 | 62   | 5.2 | 550  | 11 | US-11-184-380-14     | Sequence 14, Appl |
| 441 | 62   | 5.2 | 580  | 11 | US-11-072-512-3215   | Sequence 3215, Ap |
| 442 | 62   | 5.2 | 610  | 11 | US-11-184-380-3      | Sequence 3, Appli |
| 443 | 62   | 5.2 | 687  | 11 | US-11-072-512-2651   | Sequence 2651, Ap |
| 444 | 62   | 5.2 | 724  | 9  | US-11-188-298-321    | Sequence 321, App |
| 445 | 62   | 5.2 | 724  | 9  | US-11-079-463-321    | Sequence 321, App |
| 446 | 62   | 5.2 | 775  | 11 | US-10-469-469-322    | Sequence 322, App |
| 447 | 62   | 5.2 | 775  | 9  | US-10-973-115B-120   | Sequence 120, App |
| 448 | 62   | 5.2 | 170  | 11 | US-11-290-153-120    | Sequence 120, App |
| 449 | 62   | 5.2 | 173  | 11 | US-10-793-626-1164   | Sequence 1164, Ap |
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| 451 | 61.5 | 5.1 | 173  | 11 | US-11-172-740-2126   | Sequence 2126, Ap |
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| 927 | 58.5 | 4.9 | 354 | 11 | US-11-087-099-5563 | Sequence 5563, Ap |
| 928 | 58.5 | 4.9 | 361 | 11 | US-11-188-298-4433 | Sequence 4433, Ap |
| 929 | 58.5 | 4.9 | 361 | 9 | US-10-965-103-2 | Sequence 2, Appli |
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| 931 | 58 | 4.9 | 361 | 11 | US-11-270-717-2 | Sequence 2, Appli |
| 932 | 58 | 4.9 | 366 | 11 | US-10-455-772-2 | Sequence 2, Appli |
| 933 | 58 | 4.9 | 372 | 9 | US-10-873-528-44 | Sequence 44, Appli |
| 934 | 58 | 4.9 | 374 | 11 | US-11-188-298-13376 | Sequence 13376, A |
| 935 | 58 | 4.9 | 374 | 11 | US-11-096-568A-23913 | Sequence 23913, A |
| 936 | 58 | 4.9 | 376 | 11 | US-11-188-298-14445 | Sequence 14445, A |
| 937 | 58 | 4.9 | 388 | 11 | US-11-096-568A-6122 | Sequence 6122, Ap |
| 938 | 58 | 4.9 | 391 | 11 | US-11-188-298-8500 | Sequence 8500, Ap |
| 939 | 58 | 4.9 | 391 | 10 | US-11-096-568A-23912 | Sequence 23912, A |
| 940 | 58 | 4.9 | 394 | 11 | US-11-264-784-110 | Sequence 110, App |
| 941 | 58 | 4.9 | 394 | 11 | US-11-224-260-5 | Sequence 5, Appli |
| 942 | 58 | 4.9 | 409 | 11 | US-11-096-568A-3216 | Sequence 3216, Ap |
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| 944 | 58 | 4.9 | 421 | 11 | US-11-096-568A-17525 | Sequence 17525, A |
| 945 | 58 | 4.9 | 423 | 11 | US-11-188-298-7314 | Sequence 7314, Ap |
| 946 | 58 | 4.9 | 423 | 11 | US-11-087-099-7925 | Sequence 7925, Ap |
| 947 | 58 | 4.9 | 424 | 11 | US-11-096-568A-6121 | Sequence 6121, Ap |
| 948 | 58 | 4.9 | 425 | 9 | US-10-873-528-44 | Sequence 44, Appli |
| 949 | 58 | 4.9 | 426 | 11 | US-11-188-298-13376 | Sequence 13376, A |
| 950 | 58 | 4.9 | 439 | 11 | US-11-087-099-739 | Sequence 739, App |
| 951 | 58 | 4.9 | 463 | 11 | US-11-087-099-9885 | Sequence 9885, Ap |
| 952 | 58 | 4.9 | 463 | 11 | US-11-188-298-9134 | Sequence 9134, Ap |
| 953 | 58 | 4.9 | 469 | 11 | US-11-087-099-10242 | Sequence 10242, A |
| 954 | 58 | 4.9 | 469 | 11 | US-11-188-298-9435 | Sequence 9435, Ap |
| 955 | 58 | 4.9 | 493 | 11 | US-11-087-099-7087 | Sequence 7087, Ap |
| 956 | 58 | 4.9 | 493 | 11 | US-11-188-298-2821 | Sequence 2821, Ap |
| 957 | 58 | 4.9 | 494 | 11 | US-11-087-099-13708 | Sequence 13708, A |
| 958 | 58 | 4.9 | 550 | 11 | US-11-188-298-1809 | Sequence 1809, Ap |
| 959 | 58 | 4.9 | 571 | 11 | US-11-087-099-297 | Sequence 297, App |
| 960 | 58 | 4.9 | 596 | 11 | US-11-188-298-2675 | Sequence 2675, Ap |
| 961 | 58 | 4.9 | 616 | 9 | US-10-613-744-4 | Sequence 4, Appli |
| 962 | 58 | 4.9 | 641 | 11 | US-11-072-512-2675 | Sequence 2675, Ap |
| 963 | 58 | 4.9 | 670 | 11 | US-11-062-225-1 | Sequence 1, Appli |
| 964 | 58 | 4.9 | 670 | 11 | US-10-506-454-278 | Sequence 278, App |
| 965 | 58 | 4.9 | 697 | 8 | US-10-511-937-2939 | Sequence 2939, Ap |
| 966 | 58 | 4.9 | 718 | 9 | US-10-074-176-62 | Sequence 62, Appl |
| 967 | 58 | 4.9 | 751 | 9 | US-10-467-657-1418 | Sequence 1418, A |
| 968 | 58 | 4.9 | 821 | 11 | US-11-098-686-11418 | Sequence 11418, A |
| 969 | 58 | 4.9 | 849 | 11 | US-11-188-298-11264 | Sequence 11264, A |
| 970 | 58 | 4.9 | 923 | 11 | US-11-087-099-4257 | Sequence 4257, Ap |
| 971 | 58 | 4.9 | 923 | 11 | US-11-087-099-7810 | Sequence 7810, Ap |
| 972 | 58 | 4.9 | 923 | 11 | US-11-188-298-3244 | Sequence 3244, Ap |
| 973 | 58 | 4.9 | 923 | 11 | US-11-188-298-3978 | Sequence 3978, A |
| 974 | 58 | 4.9 | 924 | 11 | US-11-087-099-7200 | Sequence 7200, Ap |
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| 976 | 58 | 4.9 | 924 | 11 | US-11-087-099-9836 | Sequence 9836, Ap |
| 977 | 58 | 4.9 | 980 | 11 | US-11-010-239-127 | Sequence 127, App |
| 978 | 58 | 4.9 | 1049 | 11 | US-11-098-686-11239 | Sequence 11239, A |
| 979 | 58 | 4.9 | 1094 | 11 | US-11-087-099-8753 | Sequence 8753, Ap |
| 980 | 58 | 4.9 | 1163 | 11 | US-11-044-899-30 | Sequence 30, Appli |
| 981 | 58 | 4.9 | 1163 | 11 | US-11-096-568A-5993 | Sequence 5993, Ap |
| 982 | 58 | 4.9 | 101 | 11 | US-11-188-298-10446 | Sequence 10446, A |
| 983 | 58 | 4.9 | 135 | 11 | US-11-096-568A-744 | Sequence 744, App |
| 984 | 57.5 | 4.8 | 136 | 7 | US-09-978-360A-742 | Sequence 742, App |
| 985 | 57.5 | 4.8 | 142 | 8 | US-11-072-175-162 | Sequence 162, App |
| 986 | 57.5 | 4.8 | 167 | 11 | US-10-505-234-1496 | Sequence 1496, A |
| 987 | 57.5 | 4.8 | 167 | 9 | US-10-821-224-1496 | Sequence 1496, A |
| 988 | 57.5 | 4.8 | 167 | 9 | US-10-506-454-1340 | Sequence 1340, A |
| 989 | 57.5 | 4.8 | 173 | 9 | US-11-072-175-255 | Sequence 255, App |
| 990 | 57.5 | 4.8 | 313 | 11 | US-11-188-298-10140 | Sequence 10140, A |
| 991 | 57.5 | 4.8 | 324 | 11 | US-11-096-568A-1907 | Sequence 1907, A |
| 1006 | 57.5 | 4.8 | 324 | 11 | US-11-188-298-824 | Sequence 824, App |
| 1007 | 57.5 | 4.8 | 324 | 11 | US-11-188-298-6472 | Sequence 6472, Ap |
| 1008 | 57.5 | 4.8 | 326 | 11 | US-11-156-084-239 | Sequence 239, App |
| 1009 | 57.5 | 4.8 | 329 | 11 | US-10-524-647-23 | Sequence 23, Appl |
| 1010 | 57.5 | 4.8 | 329 | 9 | US-10-524-647-80 | Sequence 80, Appli |
| 1011 | 57.5 | 4.8 | 329 | 9 | US-10-524-972-23 | Sequence 23, Appl |
| 1012 | 57.5 | 4.8 | 329 | 9 | US-10-524-972-80 | Sequence 80, Appli |
| 1013 | 57.5 | 4.8 | 341 | 9 | US-10-524-972-23 | Sequence 23, Appl |
| 1014 | 57.5 | 4.8 | 341 | 9 | US-10-524-647-27 | Sequence 27, Appl |
| 1015 | 57.5 | 4.8 | 347 | 11 | US-10-524-647-80 | Sequence 80, Appli |
| 1016 | 57.5 | 4.8 | 353 | 11 | US-11-096-568A-21906 | Sequence 21906, A |
| 1017 | 57.5 | 4.8 | 353 | 11 | US-11-096-568A-9002 | Sequence 9002, Ap |
| 1018 | 57.5 | 4.8 | 353 | 11 | US-11-096-568A-9003 | Sequence 9003, Ap |

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| 1019 | 57.5 | 4.8 | 356 | 11 | US-11-096-568A-9001 | Sequence 9001, Ap |
| 1020 | 57.5 | 4.8 | 359 | 8 | US-10-511-937-2990 | Sequence 2990, App |
| 1021 | 57.5 | 4.8 | 363 | 11 | US-10-511-084-199 | Sequence 199, App |
| 1022 | 57.5 | 4.8 | 373 | 11 | US-11-044-051-71 | Sequence 71, Appl |
| 1023 | 57.5 | 4.8 | 373 | 11 | US-11-044-051-105 | Sequence 105, App |
| 1024 | 57.5 | 4.8 | 375 | 9 | US-10-469-469-115 | Sequence 115, App |
| 1025 | 57.5 | 4.8 | 377 | 11 | US-11-079-463-5276 | Sequence 5276, Ap |
| 1026 | 57.5 | 4.8 | 385 | 11 | US-11-079-463-8385 | Sequence 8385, Ap |
| 1027 | 57.5 | 4.8 | 393 | 11 | US-11-087-099-4015 | Sequence 4015, Ap |
| 1028 | 57.5 | 4.8 | 403 | 9 | US-10-523-477-11 | Sequence 11, Appl |
| 1029 | 57.5 | 4.8 | 403 | 9 | US-10-770-726-83 | Sequence 83, Appl |
| 1030 | 57.5 | 4.8 | 403 | 9 | US-10-770-726-85 | Sequence 85, Appl |
| 1031 | 57.5 | 4.8 | 403 | 9 | US-10-511-903-24 | Sequence 24, Appl |
| 1032 | 57.5 | 4.8 | 403 | 9 | US-10-511-903-12 | Sequence 12, Appl |
| 1033 | 57.5 | 4.8 | 403 | 11 | US-11-109-156-12 | Sequence 12, Appl |
| 1034 | 57.5 | 4.8 | 404 | 11 | US-11-092-168-1 | Sequence 1, Appli |
| 1035 | 57.5 | 4.8 | 408 | 11 | US-11-188-299-10310 | Sequence 10310, A |
| 1036 | 57.5 | 4.8 | 417 | 11 | US-11-096-568A-29868 | Sequence 29868, A |
| 1037 | 57.5 | 4.8 | 418 | 11 | US-11-096-568A-25551 | Sequence 25551, A |
| 1038 | 57.5 | 4.8 | 426 | 11 | US-11-079-463-9095 | Sequence 9095, Ap |
| 1039 | 57.5 | 4.8 | 434 | 11 | US-11-098-686-10155 | Sequence 10155, A |
| 1040 | 57.5 | 4.8 | 459 | 10 | US-11-302-678-11 | Sequence 11, Appl |
| 1041 | 57.5 | 4.8 | 471 | 11 | US-11-087-099-4797 | Sequence 4797, Ap |
| 1042 | 57.5 | 4.8 | 471 | 11 | US-11-188-299-15411 | Sequence 15411, A |
| 1043 | 57.5 | 4.8 | 477 | 11 | US-11-087-099-2487 | Sequence 2487, Ap |
| 1044 | 57.5 | 4.8 | 482 | 11 | US-11-096-568A-8410 | Sequence 8410, Ap |
| 1045 | 57.5 | 4.8 | 483 | 11 | US-11-188-298-1003 | Sequence 1003, Ap |
| 1046 | 57.5 | 4.8 | 519 | 11 | US-11-079-463-9938 | Sequence 9938, Ap |
| 1047 | 57.5 | 4.8 | 522 | 11 | US-10-793-626-604 | Sequence 604, App |
| 1048 | 57.5 | 4.8 | 523 | 11 | US-11-188-298-1001 | Sequence 1001, Ap |
| 1049 | 57.5 | 4.8 | 523 | 11 | US-11-188-299-4151 | Sequence 4151, Ap |
| 1050 | 57.5 | 4.8 | 523 | 11 | US-11-188-298-12581 | Sequence 12581, A |
| 1051 | 57.5 | 4.8 | 527 | 9 | US-11-188-298-12948 | Sequence 12948, A |
| 1053 | 57.5 | 4.8 | 531 | 11 | US-10-506-454-692 | Sequence 692, App |
| 1058 | 57.5 | 4.8 | 531 | 11 | US-11-188-298-14335 | Sequence 14335, A |
| 1059 | 57.5 | 4.8 | 532 | 11 | US-11-166-609-22 | Sequence 22, Appl |
| 1060 | 57.5 | 4.8 | 543 | 11 | US-11-072-512-3493 | Sequence 3493, Ap |
| 1061 | 57.5 | 4.8 | 547 | 11 | US-11-096-568A-8409 | Sequence 8409, Ap |
| 1062 | 57.5 | 4.8 | 557 | 11 | US-11-096-568A-28054 | Sequence 28054, A |
| 1063 | 57.5 | 4.8 | 566 | 11 | US-11-096-568A-8408 | Sequence 8408, Ap |
| 1065 | 57.5 | 4.8 | 605 | 11 | US-10-973-115B-160 | Sequence 160, App |
| 1068 | 57.5 | 4.8 | 605 | 11 | US-11-096-568A-29177 | Sequence 29177, A |
| 1069 | 57.5 | 4.8 | 605 | 11 | US-11-290-153-160 | Sequence 160, App |
| 1070 | 57.5 | 4.8 | 696 | 11 | US-11-072-512-2225 | Sequence 2225, Ap |
| 1071 | 57.5 | 4.8 | 722 | 11 | US-11-045-004-2631 | Sequence 2631, Ap |
| 1072 | 57.5 | 4.8 | 737 | 11 | US-11-210-316-8 | Sequence 8, Appli |
| 1073 | 57.5 | 4.8 | 759 | 11 | US-11-096-568A-29177 | Sequence 29177, A |
| 1074 | 57.5 | 4.8 | 782 | 11 | US-11-096-568A-30473 | Sequence 30473, A |
| 1075 | 57.5 | 4.8 | 782 | 11 | US-11-188-299-19923 | Sequence 19923, A |
| 1076 | 57.5 | 4.8 | 807 | 11 | US-11-079-463-5963 | Sequence 5963, Ap |
| 1077 | 57.5 | 4.8 | 874 | 11 | US-11-096-568A-29176 | Sequence 29176, A |
| 1078 | 57.5 | 4.8 | 897 | 11 | US-11-096-568A-30472 | Sequence 30472, A |
| 1079 | 57.5 | 4.8 | 1104 | 11 | US-11-188-298-17339 | Sequence 17339, A |
| 1080 | 57.5 | 4.8 | 1161 | 11 | US-10-784-004-389 | Sequence 389, App |
| 1081 | 57.5 | 4.8 | 1161 | 9 | US-10-784-004-936 | Sequence 936, App |
| 1082 | 57.5 | 4.8 | 1167 | 9 | US-10-455-772-986 | Sequence 986, App |
| 1083 | 57.5 | 4.8 | 1167 | 9 | US-10-455-772-990 | Sequence 990, App |
| 1084 | 57.5 | 4.8 | 1167 | 9 | US-10-455-772-992 | Sequence 992, App |
| 1085 | 57.5 | 4.8 | 1204 | 11 | US-11-188-298-988 | Sequence 988, App |
| 1086 | 57.5 | 4.8 | 1210 | 11 | US-11-108-172-692 | Sequence 692, App |
| 1087 | 57.5 | 4.8 | 1229 | 11 | US-11-108-172-107 | Sequence 107, App |
| 1088 | 57.5 | 4.8 | 1234 | 9 | US-10-517-939-306 | Sequence 306, App |
| 1089 | 57.5 | 4.8 | 1548 | 11 | US-11-108-172-1095 | Sequence 1095, Ap |
| 1090 | 57.5 | 4.8 | 3460 | 8 | US-10-505-928-104 | Sequence 104, App |
| 1091 | 57.5 | 4.8 | 3674 | 11 | US-11-000-463-454 | Sequence 454, Appl |
| 1092 | 57.5 | 4.8 | 7102 | 11 | US-11-143-980-48 | Sequence 48, Appl |
| 1093 | 57.5 | 4.8 | 110 | 9 | US-10-986-405-239 | Sequence 239, App |
| 1094 | 57.5 | 4.8 | 114 | 11 | US-11-172-740-628 | Sequence 628, App |
| 1095 | 57.5 | 4.8 | 126 | 9 | US-10-492-570-1925 | Sequence 1925, A |
| 1096 | 57.5 | 4.8 | 135 | 11 | US-11-054-281-107 | Sequence 107, App |
| 1097 | 57.5 | 4.8 | 141 | 11 | US-11-055-822-728 | Sequence 728, App |
| 1098 | 57.5 | 4.8 | 162 | 11 | US-11-264-096-1945 | Sequence 1945, Ap |
| 1099 | 57 | 4.8 | 174 | 11 | US-11-079-463-10145 | Sequence 10145, A |

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| 1100 | 57 | 4.8 | 180 | 11 | US-11-096-568A-11708 | Sequence 11708, A |
| 1101 | 57 | 4.8 | 191 | 11 | US-11-096-568A-11707 | Sequence 11707, A |
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| 1104 | 57 | 4.8 | 246 | 11 | US-11-188-298-8189 | Sequence 8189, Ap |
| 1105 | 57 | 4.8 | 256 | 9 | US-10-467-657-2288 | Sequence 2288, Ap |
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| 1107 | 57 | 4.8 | 270 | 11 | US-11-045-004-2432 | Sequence 2432, Ap |
| 1108 | 57 | 4.8 | 275 | 11 | US-11-188-298-18814 | Sequence 18814, A |
| 1109 | 57 | 4.8 | 283 | 11 | US-11-188-298-10214 | Sequence 10214, A |
| 1110 | 57 | 4.8 | 284 | 11 | US-11-096-568A-15523 | Sequence 15523, A |
| 1111 | 57 | 4.8 | 293 | 11 | US-11-096-568A-15522 | Sequence 15522, A |
| 1112 | 57 | 4.8 | 293 | 11 | US-11-172-740-2147 | Sequence 2147, Ap |
| 1113 | 57 | 4.8 | 294 | 11 | US-11-045-004-1428 | Sequence 1428, Ap |
| 1114 | 57 | 4.8 | 306 | 11 | US-11-096-568A-27556 | Sequence 27556, A |
| 1115 | 57 | 4.8 | 314 | 11 | US-11-172-740-378 | Sequence 378, App |
| 1116 | 57 | 4.8 | 314 | 9 | US-10-455-772-380 | Sequence 380, App |
| 1117 | 57 | 4.8 | 317 | 11 | US-11-096-568A-9345 | Sequence 9345, Ap |
| 1118 | 57 | 4.8 | 321 | 11 | US-11-096-568A-13758 | Sequence 13758, A |
| 1119 | 57 | 4.8 | 339 | 11 | US-11-096-568A-28918 | Sequence 28918, A |
| 1120 | 57 | 4.8 | 346 | 9 | US-10-793-626-1694 | Sequence 1694, Ap |
| 1121 | 57 | 4.8 | 351 | 11 | US-11-079-463-8068 | Sequence 8068, Ap |
| 1122 | 57 | 4.8 | 351 | 11 | US-11-098-686-10292 | Sequence 10292, A |
| 1123 | 57 | 4.8 | 355 | 11 | US-11-132-864-34 | Sequence 34, Appl |
| 1124 | 57 | 4.8 | 355 | 11 | US-11-188-298-20319 | Sequence 20319, A |
| 1125 | 57 | 4.8 | 357 | 11 | US-11-096-568A-15521 | Sequence 15521, A |
| 1126 | 57 | 4.8 | 361 | 11 | US-11-166-412-56 | Sequence 56, Appl |
| 1127 | 57 | 4.8 | 370 | 11 | US-11-098-686-10292 | Sequence 10292, A |
| 1128 | 57 | 4.8 | 375 | 11 | US-11-188-298-20319 | Sequence 20319, A |
| 1129 | 57 | 4.8 | 377 | 11 | US-11-188-298-11348 | Sequence 11348, A |
| 1130 | 57 | 4.8 | 382 | 11 | US-11-079-463-5992 | Sequence 5992, Ap |
| 1131 | 57 | 4.8 | 382 | 11 | US-11-055-822-670 | Sequence 670, App |
| 1132 | 57 | 4.8 | 394 | 11 | US-10-763-712A-25 | Sequence 25, Appl |
| 1133 | 57 | 4.8 | 415 | 9 | US-11-098-686-10684 | Sequence 10684, A |
| 1134 | 57 | 4.8 | 419 | 11 | US-11-096-568A-19366 | Sequence 19366, A |
| 1135 | 57 | 4.8 | 419 | 11 | US-11-304-129-47 | Sequence 47, Appl |
| 1136 | 57 | 4.8 | 421 | 10 | US-11-126-313-35 | Sequence 35, Appl |
| 1137 | 57 | 4.8 | 430 | 11 | US-11-126-313-36 | Sequence 36, Appl |
| 1138 | 57 | 4.8 | 430 | 11 | US-10-763-712A-25 | Sequence 25, Appl |
| 1139 | 57 | 4.8 | 436 | 9 | US-11-068-859-92 | Sequence 92, Appl |
| 1140 | 57 | 4.8 | 436 | 11 | US-11-068-859-90 | Sequence 90, Appl |
| 1141 | 57 | 4.8 | 444 | 11 | US-11-068-859-91 | Sequence 91, Appl |
| 1142 | 57 | 4.8 | 444 | 11 | US-11-068-859-88 | Sequence 88, Appl |
| 1143 | 57 | 4.8 | 444 | 11 | US-11-068-859-89 | Sequence 89, Appl |
| 1144 | 57 | 4.8 | 444 | 11 | US-10-015-540-6 | Sequence 6, Appli |
| 1145 | 57 | 4.8 | 454 | 9 | US-10-753-195-8 | Sequence 8, Appli |
| 1146 | 57 | 4.8 | 454 | 9 | US-11-072-512-3155 | Sequence 3155, Ap |
| 1147 | 57 | 4.8 | 454 | 11 | US-11-068-859-3 | Sequence 3, Appli |
| 1148 | 57 | 4.8 | 454 | 11 | US-11-068-859-7 | Sequence 7, Appli |
| 1149 | 57 | 4.8 | 454 | 11 | US-11-068-859-9 | Sequence 9, Appli |
| 1150 | 57 | 4.8 | 454 | 11 | US-11-068-859-19 | Sequence 19, Appl |
| 1151 | 57 | 4.8 | 454 | 11 | US-11-068-859-21 | Sequence 21, Appl |
| 1152 | 57 | 4.8 | 454 | 11 | US-11-068-859-23 | Sequence 23, Appl |
| 1153 | 57 | 4.8 | 454 | 11 | US-11-068-859-25 | Sequence 25, Appl |
| 1154 | 57 | 4.8 | 454 | 11 | US-11-068-859-27 | Sequence 27, Appl |
| 1155 | 57 | 4.8 | 454 | 11 | US-11-068-859-29 | Sequence 29, Appl |
| 1156 | 57 | 4.8 | 454 | 11 | US-11-068-859-31 | Sequence 31, Appl |
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| 1159 | 57 | 4.8 | 454 | 11 | US-11-068-859-37 | Sequence 37, Appl |
| 1160 | 57 | 4.8 | 454 | 11 | US-11-068-859-39 | Sequence 39, Appl |
| 1161 | 57 | 4.8 | 454 | 11 | US-11-068-859-78 | Sequence 78, Appl |
| 1162 | 57 | 4.8 | 454 | 11 | US-11-068-859-84 | Sequence 84, Appl |
| 1163 | 57 | 4.8 | 454 | 11 | US-11-068-859-85 | Sequence 85, Appl |
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| 1165 | 57 | 4.8 | 454 | 11 | US-11-068-859-160 | Sequence 160, App |
| 1166 | 57 | 4.8 | 454 | 11 | US-11-068-859-161 | Sequence 161, App |
| 1167 | 57 | 4.8 | 454 | 11 | US-11-068-859-162 | Sequence 162, App |
| 1168 | 57 | 4.8 | 454 | 11 | US-11-068-859-166 | Sequence 166, App |
| 1169 | 57 | 4.8 | 454 | 11 | US-11-068-859-167 | Sequence 167, App |
| 1170 | 57 | 4.8 | 454 | 11 | US-11-068-859-168 | Sequence 168, App |
| 1171 | 57 | 4.8 | 454 | 11 | US-11-068-859-173 | Sequence 173, App |
| 1172 | 57 | 4.8 | 454 | 11 | US-11-068-859-173 | Sequence 173, App |

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| 1173 | 57 | 4.8 | 454 | 11 | US-11-068-859-179 | Sequence 179, App |
| 1174 | 57 | 4.8 | 454 | 11 | US-11-068-859-185 | Sequence 185, App |
| 1175 | 57 | 4.8 | 454 | 11 | US-11-068-859-191 | Sequence 191, App |
| 1176 | 57 | 4.8 | 454 | 11 | US-11-068-859-193 | Sequence 193, App |
| 1177 | 57 | 4.8 | 459 | 9 | US-10-506-454-188 | Sequence 188, App |
| 1178 | 57 | 4.8 | 466 | 11 | US-11-087-099-10294 | Sequence 10294, A |
| 1179 | 57 | 4.8 | 469 | 11 | US-11-222-138A-18 | Sequence 18, Appl |
| 1180 | 57 | 4.8 | 471 | 9 | US-10-467-657-6022 | Sequence 6022, Appli |
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| 1183 | 57 | 4.8 | 491 | 11 | US-11-087-099-9280 | Sequence 9280, App |
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| 1185 | 57 | 4.8 | 502 | 11 | US-11-188-298-18769 | Sequence 18769, A |
| 1186 | 57 | 4.8 | 505 | 11 | US-11-079-463-8719 | Sequence 8719, Ap |
| 1187 | 57 | 4.8 | 516 | 11 | US-10-455-772-1004 | Sequence 1004, Ap |
| 1188 | 57 | 4.8 | 516 | 9 | US-11-072-512-2033 | Sequence 2033, Ap |
| 1189 | 57 | 4.8 | 522 | 9 | US-10-455-772-1002 | Sequence 1002, Ap |
| 1190 | 57 | 4.8 | 522 | 11 | US-11-045-004-1066 | Sequence 1066, App |
| 1191 | 57 | 4.8 | 525 | 11 | US-11-455-772-994 | Sequence 994, App |
| 1192 | 57 | 4.8 | 540 | 11 | US-11-485-517-223 | Sequence 223, App |
| 1193 | 57 | 4.8 | 553 | 11 | US-11-188-298-16884 | Sequence 16884, A |
| 1194 | 57 | 4.8 | 554 | 11 | US-11-096-568A-19364 | Sequence 19364, A |
| 1195 | 57 | 4.8 | 568 | 9 | US-10-455-772-994 | Sequence 994, App |
| 1196 | 57 | 4.8 | 576 | 11 | US-11-188-298-21533 | Sequence 21533, A |
| 1197 | 57 | 4.8 | 596 | 11 | US-11-188-298-1420 | Sequence 1420, Ap |
| 1198 | 57 | 4.8 | 601 | 11 | US-11-045-004-480 | Sequence 480, App |
| 1199 | 57 | 4.8 | 655 | 11 | US-11-188-298-14574 | Sequence 14574, A |
| 1200 | 57 | 4.8 | 692 | 9 | US-10-928-446A-9802 | Sequence 9802, Ap |
| 1201 | 57 | 4.8 | 721 | 11 | US-11-072-512-3212 | Sequence 3212, Ap |
| 1202 | 57 | 4.8 | 732 | 11 | US-11-188-298-668 | Sequence 668, App |
| 1203 | 57 | 4.8 | 761 | 11 | US-11-096-568A-27816 | Sequence 27816, A |
| 1204 | 57 | 4.8 | 776 | 11 | US-11-096-568A-27815 | Sequence 27815, A |
| 1205 | 57 | 4.8 | 798 | 9 | US-11-107-028-2 | Sequence 2, Appli |
| 1206 | 57 | 4.8 | 802 | 11 | US-11-045-004-2796 | Sequence 2796, Ap |
| 1207 | 57 | 4.8 | 824 | 9 | US-10-330-773-110 | Sequence 110, App |
| 1208 | 57 | 4.8 | 824 | 9 | US-11-045-004-1086 | Sequence 1086, Ap |
| 1209 | 57 | 4.8 | 834 | 9 | US-10-928-446A-6182 | Sequence 6182, Ap |
| 1210 | 57 | 4.8 | 834 | 9 | US-10-928-446A-194 | Sequence 194, App |
| 1211 | 57 | 4.8 | 834 | 9 | US-10-928-446A-196 | Sequence 196, App |
| 1212 | 57 | 4.8 | 834 | 9 | US-10-928-446A-198 | Sequence 198, App |
| 1213 | 57 | 4.8 | 834 | 9 | US-10-928-446A-200 | Sequence 200, App |
| 1214 | 57 | 4.8 | 834 | 9 | US-10-928-446A-202 | Sequence 202, App |
| 1215 | 57 | 4.8 | 839 | 11 | US-11-096-568A-27814 | Sequence 27814, A |
| 1216 | 57 | 4.8 | 879 | 11 | US-11-087-099-6182 | Sequence 6182, Ap |
| 1217 | 57 | 4.8 | 924 | 11 | US-11-087-099-16679 | Sequence 16679, A |
| 1218 | 57 | 4.8 | 924 | 11 | US-11-087-099-1558 | Sequence 1558, Ap |
| 1219 | 57 | 4.8 | 925 | 11 | US-11-087-099-3884 | Sequence 3884, Ap |
| 1220 | 57 | 4.8 | 925 | 11 | US-11-928-446A-184 | Sequence 184, App |
| 1221 | 57 | 4.8 | 925 | 11 | US-11-188-298-14632 | Sequence 14632, A |
| 1222 | 57 | 4.8 | 925 | 11 | US-11-928-446A-186 | Sequence 186, App |
| 1223 | 57 | 4.8 | 933 | 11 | US-10-330-773-108 | Sequence 108, App |
| 1224 | 57 | 4.8 | 942 | 11 | US-11-188-298-19329 | Sequence 19329, A |
| 1225 | 57 | 4.8 | 946 | 11 | US-10-330-773-106 | Sequence 106, App |
| 1226 | 57 | 4.8 | 947 | 9 | US-10-928-446A-190 | Sequence 190, App |
| 1227 | 57 | 4.8 | 948 | 9 | US-10-330-773-104 | Sequence 104, App |
| 1228 | 57 | 4.8 | 950 | 9 | US-10-928-446A-182 | Sequence 182, App |
| 1229 | 57 | 4.8 | 955 | 9 | US-10-928-446A-186 | Sequence 186, App |
| 1230 | 57 | 4.8 | 990 | 9 | US-10-330-773-108 | Sequence 108, App |
| 1231 | 57 | 4.8 | 1160 | 11 | US-11-188-298-19329 | Sequence 19329, A |
| 1232 | 57 | 4.8 | 1224 | 11 | US-11-096-568A-27547 | Sequence 27547, A |
| 1233 | 57 | 4.8 | 1236 | 11 | US-11-096-568A-27546 | Sequence 27546, A |
| 1234 | 57 | 4.8 | 1240 | 11 | US-11-096-568A-27545 | Sequence 27545, A |
| 1235 | 57 | 4.8 | 2004 | 9 | US-10-982-440-62 | Sequence 62, Appl |
| 1236 | 57 | 4.8 | 107 | 9 | US-10-469-469-250 | Sequence 250, App |
| 1237 | 57 | 4.8 | 108 | 11 | US-11-049-536-260 | Sequence 260, App |
| 1238 | 57 | 4.8 | 108 | 11 | US-11-199-739-260 | Sequence 260, App |
| 1239 | 57 | 4.8 | 114 | 11 | US-11-096-568A-21191 | Sequence 21191, A |
| 1240 | 57 | 4.8 | 155 | 11 | US-11-264-096-1220 | Sequence 1220, Ap |
| 1241 | 57 | 4.8 | 178 | 11 | US-11-188-298-8788 | Sequence 8788, Ap |
| 1242 | 57 | 4.7 | 183 | 11 | US-11-188-298-8788 | Sequence 8788, Ap |
| 1243 | 57 | 4.7 | 200 | 11 | US-11-167-831-35 | Sequence 35, Appl |
| 1244 | 57 | 4.7 | 201 | 11 | US-11-167-831-39 | Sequence 39, Appl |
| 1245 | 56.5 | 4.7 | 241 | 9 | US-10-506-454-1423 | Sequence 1423, Ap |

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| 1246 | 56.5 | 4.7 | 269 | 9 | US-10-986-405-201 | Sequence 201, App |
| 1247 | 56.5 | 4.7 | 273 | 9 | US-10-644-907-231 | Sequence 231, App |
| 1248 | 56.5 | 4.7 | 280 | 11 | US-10-745-586-71 | Sequence 71, Appl |
| 1249 | 56.5 | 4.7 | 292 | 9 | US-11-079-463-6326 | Sequence 6326, Ap |
| 1250 | 56.5 | 4.7 | 295 | 11 | US-11-188-298-4689 | Sequence 4689, App |
| 1251 | 56.5 | 4.7 | 308 | 11 | US-11-045-004-2222 | Sequence 2222, Ap |
| 1252 | 56.5 | 4.7 | 310 | 11 | US-11-096-568A-12784 | Sequence 12784, A |
| 1253 | 56.5 | 4.7 | 310 | 11 | US-11-096-568A-33921 | Sequence 33921, A |
| 1254 | 56.5 | 4.7 | 314 | 11 | US-11-096-568A-6441 | Sequence 6441, Ap |
| 1255 | 56.5 | 4.7 | 322 | 9 | US-10-523-503-58 | Sequence 58, Appl |
| 1256 | 56.5 | 4.7 | 322 | 11 | US-11-096-568A-33920 | Sequence 33920, A |
| 1257 | 56.5 | 4.7 | 322 | 11 | US-11-096-568A-33919 | Sequence 33919, A |
| 1258 | 56.5 | 4.7 | 322 | 11 | US-11-188-298-1018 | Sequence 1018, Ap |
| 1259 | 56.5 | 4.7 | 325 | 11 | US-11-188-298-13208 | Sequence 13208, A |
| 1260 | 56.5 | 4.7 | 325 | 11 | US-11-079-463-6582 | Sequence 6582, Ap |
| 1261 | 56.5 | 4.7 | 329 | 9 | US-10-524-647-2 | Sequence 2, Appli |
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| 1264 | 56.5 | 4.7 | 331 | 9 | US-10-523-503-58 | Sequence 58, Appl |
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| 1266 | 56.5 | 4.7 | 344 | 11 | US-11-174-819-79 | Sequence 79, Appl |
| 1267 | 56.5 | 4.7 | 347 | 11 | US-11-174-819-76 | Sequence 76, Appl |
| 1268 | 56.5 | 4.7 | 357 | 11 | US-11-261-135-2 | Sequence 2, Appli |
| 1269 | 56.5 | 4.7 | 357 | 11 | US-11-506-454-770 | Sequence 770, App |
| 1270 | 56.5 | 4.7 | 359 | 9 | US-10-055-877-272 | Sequence 272, App |
| 1271 | 56.5 | 4.7 | 376 | 9 | US-10-203-486-5 | Sequence 5, Appli |
| 1272 | 56.5 | 4.7 | 384 | 9 | US-10-784-004-367 | Sequence 367, App |
| 1273 | 56.5 | 4.7 | 386 | 11 | US-11-055-822-586 | Sequence 586, App |
| 1274 | 56.5 | 4.7 | 391 | 11 | US-11-072-512-2911 | Sequence 2911, Ap |
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| 1276 | 56.5 | 4.7 | 397 | 11 | US-11-045-004-106 | Sequence 106, App |
| 1277 | 56.5 | 4.7 | 398 | 11 | US-11-096-568A-18324 | Sequence 18324, A |
| 1278 | 56.5 | 4.7 | 401 | 11 | US-11-087-099-10037 | Sequence 10037, A |
| 1279 | 56.5 | 4.7 | 416 | 11 | US-11-096-568A-18081 | Sequence 18081, A |
| 1280 | 56.5 | 4.7 | 416 | 11 | US-11-096-568A-26755 | Sequence 26755, A |
| 1281 | 56.5 | 4.7 | 419 | 11 | US-11-096-568A-26754 | Sequence 26754, A |
| 1282 | 56.5 | 4.7 | 426 | 11 | US-11-115-877-2 | Sequence 2, Appli |
| 1283 | 56.5 | 4.7 | 426 | 11 | US-11-186-284-89 | Sequence 89, Appl |
| 1284 | 56.5 | 4.7 | 426 | 11 | US-11-096-568A-16741 | Sequence 16741, A |
| 1285 | 56.5 | 4.7 | 433 | 11 | US-11-188-298-14554 | Sequence 14554, A |
| 1286 | 56.5 | 4.7 | 436 | 11 | US-11-050-857-566 | Sequence 566, App |
| 1287 | 56.5 | 4.7 | 439 | 11 | US-11-087-099-3719 | Sequence 3719, Ap |
| 1288 | 56.5 | 4.7 | 443 | 11 | US-11-087-099-2428 | Sequence 2428, Ap |
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| 1291 | 56.5 | 4.7 | 446 | 11 | US-11-096-568A-12783 | Sequence 12783, A |
| 1292 | 56.5 | 4.7 | 452 | 11 | US-11-087-099-19991 | Sequence 19991, A |
| 1293 | 56.5 | 4.7 | 452 | 11 | US-11-087-099-9683 | Sequence 9683, Ap |
| 1294 | 56.5 | 4.7 | 456 | 11 | US-11-188-298-18080 | Sequence 18080, A |
| 1295 | 56.5 | 4.7 | 461 | 11 | US-11-096-568A-18323 | Sequence 18323, A |
| 1296 | 56.5 | 4.7 | 461 | 11 | US-11-188-298-14715 | Sequence 14715, A |
| 1297 | 56.5 | 4.7 | 463 | 11 | US-11-188-298-1923 | Sequence 1923, Ap |
| 1298 | 56.5 | 4.7 | 463 | 11 | US-11-096-568A-2513 | Sequence 2513, Ap |
| 1299 | 56.5 | 4.7 | 463 | 11 | US-11-096-568A-6433 | Sequence 6433, Ap |
| 1300 | 56.5 | 4.7 | 463 | 11 | US-11-087-099-9945 | Sequence 9945, Ap |
| 1301 | 56.5 | 4.7 | 463 | 11 | US-11-188-298-2840 | Sequence 2840, Ap |
| 1302 | 56.5 | 4.7 | 463 | 11 | US-11-188-298-1518 | Sequence 1518, Ap |
| 1303 | 56.5 | 4.7 | 463 | 11 | US-11-096-568A-18518 | Sequence 18518, A |
| 1304 | 56.5 | 4.7 | 470 | 11 | US-11-188-298-19286 | Sequence 19286, A |
| 1305 | 56.5 | 4.7 | 473 | 11 | US-11-188-298-14715 | Sequence 14715, A |
| 1306 | 56.5 | 4.7 | 476 | 11 | US-11-096-568A-18079 | Sequence 18079, A |
| 1307 | 56.5 | 4.7 | 476 | 11 | US-11-188-298-1923 | Sequence 1923, Ap |
| 1308 | 56.5 | 4.7 | 480 | 11 | US-11-096-568A-12782 | Sequence 12782, A |
| 1309 | 56.5 | 4.7 | 486 | 11 | US-11-087-099-8629 | Sequence 8629, Ap |
| 1310 | 56.5 | 4.7 | 486 | 11 | US-11-096-568A-19034 | Sequence 19034, A |
| 1311 | 56.5 | 4.7 | 491 | 11 | US-11-087-099-10403 | Sequence 10403, A |
| 1312 | 56.5 | 4.7 | 491 | 11 | US-11-096-568A-9602 | Sequence 9602, Ap |
| 1313 | 56.5 | 4.7 | 520 | 11 | US-11-096-568A-18322 | Sequence 18322, A |
| 1314 | 56.5 | 4.7 | 546 | 11 | US-11-188-298-319 | Sequence 319, App |
| 1315 | 56.5 | 4.7 | 567 | 11 | US-11-079-463-9801 | Sequence 9801, Ap |
| 1316 | 56.5 | 4.7 | 580 | 11 | US-11-079-463-9001 | Sequence 9001, Ap |
| 1317 | 56.5 | 4.7 | 580 | 11 | US-11-188-298-9465 | Sequence 9465, Ap |
| 1318 | 56.5 | 4.7 | 585 | 11 | US-11-188-298-18257 | Sequence 18257, A |
| | | | | 11 | US-11-188-298-18531 | Sequence 18531, A |

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| 1319 | 56.5 | 4.7 | 586 | 11 | US-11-072-512-3411 | Sequence 3411, Ap |
| 1320 | 56.5 | 4.7 | 618 | 11 | US-11-188-298-20392 | Sequence 20392, A |
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| 1322 | 56.5 | 4.7 | 620 | 11 | US-11-188-299-4227 | Sequence 4227, Ap |
| 1323 | 56.5 | 4.7 | 628 | 11 | US-11-045-004-807 | Sequence 807, Appl |
| 1324 | 56.5 | 4.7 | 649 | 11 | US-11-188-298-3484 | Sequence 3484, App |
| 1325 | 56.5 | 4.7 | 662 | 11 | US-11-188-298-13798 | Sequence 13798, A |
| 1326 | 56.5 | 4.7 | 670 | 11 | US-11-079-463-5950 | Sequence 5950, Ap |
| 1327 | 56.5 | 4.7 | 674 | 9 | US-10-467-657-6812 | Sequence 6812, Ap |
| 1328 | 56.5 | 4.7 | 730 | 9 | US-10-703-799B-218 | Sequence 218, App |
| 1329 | 56.5 | 4.7 | 730 | 11 | US-11-082-389-358 | Sequence 358, App |
| 1330 | 56.5 | 4.7 | 761 | 9 | US-10-915-002-184 | Sequence 184, App |
| 1331 | 56.5 | 4.7 | 784 | 11 | US-11-072-175-153 | Sequence 153, App |
| 1332 | 56.5 | 4.7 | 796 | 11 | US-11-188-298-10947 | Sequence 10947, A |
| 1333 | 56.5 | 4.7 | 817 | 11 | US-11-072-512-2301 | Sequence 2301, Ap |
| 1334 | 56.5 | 4.7 | 852 | 11 | US-11-072-512-3646 | Sequence 3646, Ap |
| 1335 | 56.5 | 4.7 | 858 | 9 | US-10-878-556A-113 | Sequence 113, App |
| 1336 | 56.5 | 4.7 | 864 | 11 | US-11-188-298-19464 | Sequence 19464, A |
| 1337 | 56.5 | 4.7 | 885 | 11 | US-11-188-298-13076 | Sequence 13076, A |
| 1338 | 56.5 | 4.7 | 1066 | 11 | US-11-096-568A-9576 | Sequence 9576, Ap |
| 1339 | 56.5 | 4.7 | 1094 | 11 | US-11-098-686-10160 | Sequence 10160, A |
| 1340 | 56.5 | 4.7 | 1938 | 11 | US-11-188-298-4370 | Sequence 4370, Ap |
| 1341 | 56.5 | 4.7 | 2009 | 10 | US-11-263-326-168 | Sequence 168, App |
| 1342 | 56.5 | 4.7 | 2312 | 11 | US-11-126-313-34 | Sequence 34, Appl |
| 1343 | 56.5 | 4.7 | 2426 | 11 | US-11-188-299-15486 | Sequence 15486, A |
| 1344 | 56.5 | 4.7 | 153 | 11 | US-11-096-568A-9575 | Sequence 9575, Ap |
| 1345 | 56.5 | 4.7 | 156 | 11 | US-11-096-568A-5422 | Sequence 5422, Ap |
| 1346 | 56.5 | 4.7 | 166 | 11 | US-11-188-298-5422 | Sequence 5422, Ap |
| 1347 | 56.5 | 4.7 | 173 | 10 | US-11-507-355-3 | Sequence 3, Appli |
| 1348 | 56.5 | 4.7 | 177 | 11 | US-11-087-099-11865 | Sequence 11865, A |
| 1349 | 56.5 | 4.7 | 178 | 11 | US-11-087-099-4291 | Sequence 4291, Ap |
| 1350 | 56.5 | 4.7 | 188 | 9 | US-10-936-888-1 | Sequence 1, Appli |
| 1351 | 56.5 | 4.7 | 196 | 9 | US-10-793-626-2014 | Sequence 2014, Ap |
| 1352 | 56.5 | 4.7 | 196 | 11 | US-11-096-568A-9574 | Sequence 9574, Ap |
| 1353 | 56.5 | 4.7 | 216 | 11 | US-11-096-568A-27032 | Sequence 27032, A |
| 1354 | 56.5 | 4.7 | 216 | 11 | US-11-264-096-1114 | Sequence 1114, Ap |
| 1355 | 56.5 | 4.7 | 225 | 10 | US-11-264-096-1115 | Sequence 1115, Ap |
| 1356 | 56.5 | 4.7 | 232 | 11 | US-11-257-062-18 | Sequence 18, Appl |
| 1357 | 56.5 | 4.7 | 234 | 11 | US-11-096-568A-10994 | Sequence 10994, A |
| 1358 | 56.5 | 4.7 | 238 | 11 | US-11-096-568A-4571 | Sequence 4571, Ap |
| 1359 | 56.5 | 4.7 | 242 | 11 | US-11-087-099-5746 | Sequence 5746, Ap |
| 1360 | 56.5 | 4.7 | 248 | 11 | US-11-096-568A-2932 | Sequence 2932, Ap |
| 1361 | 56.5 | 4.7 | 258 | 11 | US-11-096-568A-4570 | Sequence 4570, Ap |
| 1362 | 56.5 | 4.7 | 262 | 9 | US-10-096-568A-10993 | Sequence 10993, A |
| 1363 | 56.5 | 4.7 | 273 | 11 | US-11-096-568A-3450 | Sequence 3450, Ap |
| 1364 | 56.5 | 4.7 | 282 | 11 | US-11-188-298-8305 | Sequence 8305, Ap |
| 1365 | 56.5 | 4.7 | 284 | 11 | US-11-087-099-8862 | Sequence 8862, Ap |
| 1366 | 56.5 | 4.7 | 286 | 11 | US-11-096-568A-4569 | Sequence 4569, Ap |
| 1367 | 56.5 | 4.7 | 291 | 11 | US-11-098-686-10890 | Sequence 10890, A |
| 1368 | 56.5 | 4.7 | 293 | 11 | US-11-188-298-342 | Sequence 342, App |
| 1369 | 56.5 | 4.7 | 303 | 9 | US-10-467-657-4834 | Sequence 4834, Ap |
| 1370 | 56.5 | 4.7 | 306 | 11 | US-11-188-298-18841 | Sequence 18841, A |
| 1371 | 56.5 | 4.7 | 308 | 11 | US-11-045-004-2097 | Sequence 2097, Ap |
| 1372 | 56.5 | 4.7 | 313 | 9 | US-10-079-463-5725 | Sequence 5725, Ap |
| 1387 | 56.5 | 4.7 | 314 | 11 | US-11-915-002-235 | Sequence 235, App |
| 1388 | 56.5 | 4.7 | 321 | 11 | US-11-096-568A-27031 | Sequence 27031, A |
| 1389 | 56.5 | 4.7 | 332 | 9 | US-10-045-004-1646 | Sequence 1646, Ap |
| 1390 | 56.5 | 4.7 | 334 | 11 | US-11-497-767-3 | Sequence 3, Appli |
| 1391 | 56.5 | 4.7 | 338 | 11 | US-11-096-568A-25716 | Sequence 25716, A |
| 1392 | 56.5 | 4.7 | 350 | 11 | US-11-079-463-7480 | Sequence 7480, Ap |
| 1393 | 56.5 | 4.7 | 362 | 9 | US-10-506-454-826 | Sequence 826, App |
| 1394 | 56.5 | 4.7 | 371 | 11 | US-11-079-463-4642 | Sequence 4642, Ap |
| 1395 | 56.5 | 4.7 | 373 | 9 | US-10-237-813-3 | Sequence 3, Appli |
| 1396 | 56.5 | 4.7 | 373 | 11 | US-11-134-811-2 | Sequence 2, Appli |
| 1397 | 56.5 | 4.7 | 373 | 9 | US-10-237-813-4 | Sequence 4, Appli |
| 1398 | 56.5 | 4.7 | 373 | 11 | US-11-218-281-1 | Sequence 1, Appli |
| 1399 | 56.5 | 4.7 | 373 | 11 | US-11-218-281-28 | Sequence 28, Appl |
| 1400 | 56.5 | 4.7 | 373 | 11 | US-11-087-099-11642 | Sequence 11642, A |
| 1401 | 56.5 | 4.7 | 373 | 11 | US-11-087-099-21819 | Sequence 21819, A |
| 1402 | 56.5 | 4.7 | 384 | 11 | US-11-098-686-10730 | Sequence 10730, A |
| 1403 | 56.5 | 4.7 | 398 | 11 | US-11-098-686-9 | Sequence 9, Appli |
| 1404 | 56 | 4.7 | 407 | 9 | US-11-046-668-9 | Sequence 14, Appl |
| 1405 | 56 | 4.7 | 407 | 9 | US-10-613-744-14 | Sequence 14, Appl |

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| 1407 | 56 | 4.7 | 408 | 11 | US-11-079-463-5601 | Sequence 5601, Ap |
| 1408 | 56 | 4.7 | 415 | 11 | US-11-096-568A-13118 | Sequence 13118, A |
| 1409 | 56 | 4.7 | 422 | 11 | US-11-188-298-6525 | Sequence 6525, Ap |
| 1410 | 56 | 4.7 | 423 | 11 | US-11-096-568A-13117 | Sequence 13117, A |
| 1411 | 56 | 4.7 | 428 | 11 | US-11-079-463-9578 | Sequence 9578, Ap |
| 1412 | 56 | 4.7 | 430 | 11 | US-11-087-099-4508 | Sequence 4508, Ap |
| 1413 | 56 | 4.7 | 435 | 11 | US-11-199-821-2 | Sequence 2, Appli |
| 1414 | 56 | 4.7 | 443 | 11 | US-11-087-099-9359 | Sequence 9359, Ap |
| 1415 | 56 | 4.7 | 443 | 11 | US-11-069-859-93 | Sequence 93, Appl |
| 1416 | 56 | 4.7 | 458 | 11 | US-11-087-099-11856 | Sequence 11856, A |
| 1417 | 56 | 4.7 | 464 | 11 | US-11-096-568A-5424 | Sequence 5424, Ap |
| 1418 | 56 | 4.7 | 468 | 11 | US-11-188-298-3764 | Sequence 3764, Ap |
| 1419 | 56 | 4.7 | 470 | 11 | US-11-096-568A-5505 | Sequence 5505, Ap |
| 1420 | 56 | 4.7 | 475 | 11 | US-11-087-099-4508 | Sequence 4508, Ap |
| 1421 | 56 | 4.7 | 475 | 11 | US-11-188-298-15161 | Sequence 15161, A |
| 1422 | 56 | 4.7 | 475 | 11 | US-11-096-568A-34294 | Sequence 34294, A |
| 1423 | 56 | 4.7 | 479 | 11 | US-11-188-298-8980 | Sequence 8980, Ap |
| 1424 | 56 | 4.7 | 479 | 11 | US-11-096-568A-20761 | Sequence 20761, A |
| 1425 | 56 | 4.7 | 489 | 11 | US-11-087-099-17510 | Sequence 17510, A |
| 1426 | 56 | 4.7 | 492 | 11 | US-11-096-568A-28202 | Sequence 28202, A |
| 1427 | 56 | 4.7 | 494 | 11 | US-11-096-568A-28722 | Sequence 28722, A |
| 1428 | 56 | 4.7 | 495 | 11 | US-11-096-568A-28201 | Sequence 28201, A |
| 1429 | 56 | 4.7 | 497 | 11 | US-11-096-568A-28721 | Sequence 28721, A |
| 1430 | 56 | 4.7 | 497 | 11 | US-11-087-099-8915 | Sequence 8915, Ap |
| 1431 | 56 | 4.7 | 503 | 11 | US-11-096-568A-28720 | Sequence 28720, A |
| 1432 | 56 | 4.7 | 503 | 11 | US-11-087-099-7853 | Sequence 7853, Ap |
| 1433 | 56 | 4.7 | 505 | 11 | US-11-096-568A-34293 | Sequence 34293, A |
| 1434 | 56 | 4.7 | 505 | 11 | US-11-096-568A-34292 | Sequence 34292, A |
| 1435 | 56 | 4.7 | 506 | 11 | US-11-188-298-20761 | Sequence 20761, A |
| 1436 | 56 | 4.7 | 507 | 11 | US-11-087-099-9490 | Sequence 9490, Ap |
| 1437 | 56 | 4.7 | 512 | 11 | US-11-096-568A-34292 | Sequence 34292, A |
| 1438 | 56 | 4.7 | 512 | 11 | US-11-188-298-22498 | Sequence 22498, A |
| 1439 | 56 | 9 | 541 | 11 | US-10-455-772-212 | Sequence 212, App |
| 1448 | 56 | 4.7 | 541 | 11 | US-11-077-619-50 | Sequence 50, Appl |
| 1449 | 56 | 4.7 | 541 | 11 | US-11-087-099-4050 | Sequence 4050, Ap |
| 1450 | 56 | 4.7 | 552 | 11 | US-11-188-298-1024 | Sequence 1024, Ap |
| 1451 | 56 | 4.7 | 556 | 11 | US-11-096-568A-28200 | Sequence 28200, A |
| 1452 | 56 | 4.7 | 556 | 11 | US-11-087-099-8042 | Sequence 8042, Ap |
| 1453 | 56 | 4.7 | 556 | 11 | US-11-188-298-7432 | Sequence 7432, Ap |
| 1454 | 56 | 4.7 | 586 | 11 | US-11-188-298-17159 | Sequence 17159, A |
| 1455 | 56 | 4.7 | 590 | 11 | US-11-054-281-93 | Sequence 93, Appl |
| 1456 | 56 | 4.7 | 593 | 11 | US-11-087-099-6096 | Sequence 6096, Ap |
| 1457 | 56 | 4.7 | 593 | 11 | US-11-188-298-3671 | Sequence 3671, Ap |
| 1458 | 56 | 4.7 | 594 | 11 | US-11-188-298-14439 | Sequence 14439, A |
| 1459 | 56 | 4.7 | 595 | 11 | US-11-087-099-9040 | Sequence 9040, Ap |
| 1460 | 56 | 4.7 | 595 | 11 | US-11-188-298-8366 | Sequence 8366, Ap |
| 1461 | 56 | 4.7 | 595 | 9 | US-10-455-772-214 | Sequence 214, App |
| 1462 | 56 | 4.7 | 595 | 9 | US-10-455-772-224 | Sequence 224, App |
| 1463 | 56 | 4.7 | 595 | 9 | US-10-455-772-226 | Sequence 226, App |
| 1464 | 56 | 4.7 | 595 | 9 | US-10-455-772-228 | Sequence 228, App |
| 1465 | 56 | 4.7 | 595 | 9 | US-10-455-772-230 | Sequence 230, App |
| 1466 | 56 | 4.7 | 595 | 9 | US-10-455-772-232 | Sequence 232, App |
| 1467 | 56 | 4.7 | 595 | 9 | US-10-455-772-238 | Sequence 238, App |
| 1468 | 56 | 4.7 | 595 | 9 | US-10-455-772-240 | Sequence 240, App |
| 1469 | 56 | 4.7 | 604 | 9 | US-10-455-772-218 | Sequence 218, App |
| 1470 | 56 | 4.7 | 604 | 9 | US-10-455-772-218 | Sequence 218, App |
| 1471 | 56 | 4.7 | 648 | 9 | US-11-087-099-4135 | Sequence 4135, Ap |
| 1472 | 56 | 4.7 | 674 | 11 | US-10-533-066-1 | Sequence 1, Appli |
| 1473 | 56 | 4.7 | 680 | 11 | US-11-245-400-27 | Sequence 27, Appl |
| 1474 | 56 | 4.7 | 680 | 9 | US-10-784-004-412 | Sequence 412, App |
| 1475 | 56 | 4.7 | 687 | 11 | US-11-079-463-9524 | Sequence 9524, Ap |
| 1476 | 56 | 4.7 | 691 | 11 | US-11-098-686-10524 | Sequence 10524, A |
| 1477 | 56 | 4.7 | 706 | 11 | US-11-098-686-8640 | Sequence 8640, Ap |
| 1478 | 56 | 4.7 | 840 | 11 | US-11-108-172-1102 | Sequence 1102, Ap |

| | | | | | |
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| 1479 | 56 | 4.7 | 11 | US-11-098-686-11082 | Sequence 11082, A |
| 1480 | 56 | 4.7 | 11 | US-11-188-298-9815 | Sequence 9815, Ap |
| 1481 | 56 | 4.7 | 11 | US-11-188-298-17468 | Sequence 17468, A |
| 1482 | 56 | 4.7 | 11 | US-11-124-367A-446 | Sequence 446, App |
| 1483 | 56 | 4.7 | 11 | US-11-126-313-33 | Sequence 33, Appl |
| 1484 | 55.5 | 4.6 | 11 | US-11-049-536-26 | Sequence 26, Appl |
| 1485 | 55.5 | 4.6 | 11 | US-11-199-739-26 | Sequence 26, Appl |
| 1486 | 55.5 | 4.6 | 11 | US-11-087-099-7114 | Sequence 7114, Ap |
| 1487 | 55.5 | 4.6 | 11 | US-11-172-740-625 | Sequence 625, App |
| 1488 | 55.5 | 4.6 | 11 | US-11-096-568A-4066 | Sequence 4066, Ap |
| 1489 | 55.5 | 4.6 | 11 | US-11-165-697-47 | Sequence 47, Appl |
| 1490 | 55.5 | 4.6 | 11 | US-11-087-099-9846 | Sequence 9846, Ap |
| 1491 | 55.5 | 4.6 | 11 | US-11-096-568A-21794 | Sequence 21794, A |
| 1492 | 55.5 | 4.6 | 9 | US-10-714-887-134 | Sequence 134, App |
| 1493 | 55.5 | 4.6 | 11 | US-11-087-099-10122 | Sequence 10122, A |
| 1494 | 55.5 | 4.6 | 11 | US-11-096-568A-21717 | Sequence 21717, A |
| 1495 | 55.5 | 4.6 | 11 | US-11-098-686-11423 | Sequence 11423, A |
| 1496 | 55.5 | 4.6 | 11 | US-11-096-568A-18338 | Sequence 18338, A |
| 1497 | 55.5 | 4.6 | 11 | US-11-087-099-1532 | Sequence 1532, Ap |
| 1498 | 55.5 | 4.6 | 11 | US-11-188-298-2598 | Sequence 2598, Ap |
| 1499 | 55.5 | 4.6 | 11 | US-11-096-568A-4065 | Sequence 4065, Ap |
| 1500 | 55.5 | 4.6 | 11 | US-11-096-568A-21716 | Sequence 21716, A |

Search completed: May 12, 2006, 21:13:39
Job time : 18 secs

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OM protein - protein search, using sw model

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          GenCore version 5.1.8

Run on:   May 12, 2006, 20:39:27 ; Search time 41 Seconds
                                    (without alignments)
                                    549.140 Million cell updates/sec

Title:         US-10-063-518-14
Perfect score: 1195
Sequence:      1 MNHLPEDMENALTGSQSSHA.........EAGSEEAEEKQDSEKPLLEL 234
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
Searched:      283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:  283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :  PIR_80:*
         1: pir1:*
         2: pir2:*
         3: pir3:*
         4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	664	55.6	445	2	I38027	MLN 64 protein - h
2	204	17.1	478	2	T16170	hypothetical prote
3	102.5	8.6	348	2	H90281	hypothetical prote
4	93.5	7.8	424	2	D75080	glucose-1-phosphat
5	90	7.5	1911	2	T43048	calcium channel al
6	86.5	7.2	767	2	T21969	hypothetical prote
7	85.5	7.2	396	2	B81299	probable molybdopt
8	85.5	7.2	438	2	A57219	Batten disease-rel
9	85	7.1	448	2	G70172	conserved hypothet
10	84.5	7.1	471	2	A41680	integral membrane
11	83.5	7.0	352	2	H97002	probable integral
12	83	6.9	291	2	AE0302	sugar ABC transpor
13	83	6.9	590	1	S34960	NADH2 dehydrogenas
14	82.5	6.9	186	2	B29835	TraS protein - Esc
15	82.5	6.9	239	1	C64227	hypothetical prote
16	82.5	6.9	341	2	S51265	probable N-acetylg
17	82.5	6.9	406	2	T43120	conserved hypothet
18	82.5	6.9	891	2	T37397	major core protein
19	82	6.9	589	2	T52070	RNA1 protein homol
20	82	6.9	589	2	A36983	RNA1 homolog fug1
21	81	6.8	1466	2	T30566	ATP-binding casset
22	81	6.8	385	2	B84447	hypothetical prote
23	81	6.8	529	2	T23190	probable membrane
24	81	6.8	532	2	S46831	probable membrane
25	80.5	6.7	156	2	T45568	melatonin receptor
26	80.5	6.7	322	2	I84498	hypothetical prote
27	80.5	6.7	396	2	T50229	probable transmemb
28	80.5	6.7	417	2	C44038	tryptophan permeas
29	80.5	6.7	463	2	AE1155	amino acid transpo
30	80.5	6.7	536	2	A71491	probable integral
31	80.5	6.7	644	2	S63056	probable membrane
32	80.5	6.7	738	2	S10659	membrane protein t
33	80.5	6.7	891	2	WMVZ3S	major core protein
34	80.5	6.7	891	1	WMVZ3W	major core protein
35	80.5	6.7	1780	2	A85045	probable glucan sy
36	80	6.7	103	2	G75513	conserved hypothet
37	80	6.7	290	2	D89898	hypothetical prote
38	80	6.7	309	2	S59140	RTM1 protein - yea
39	80	6.7	388	2	H71115	hypothetical prote
40	80	6.7	1339	2	A84681	probable SNF2 subf
41	79.5	6.7	463	2	AH1513	amino acid transpo
42	79.5	6.7	491	1	EDBEIC	immediate-early pr
43	78.5	6.6	239	2	S73812	hypothetical prote
44	78.5	6.6	269	2	AF1532	spermidine/putresc
45	78.5	6.6	358	2	F64136	spermidine/putresc
46	78.5	6.6	471	2	S11280	rnfd protein homol
47	78.5	6.6	678	2	S44925	serotonin receptor
48	78	6.6	245	2	JC5346	IB3/5-polypeptide
49	78	6.6	259	2	E97157	cdd2 protein - Clo
50	78	6.6	382	2	F83825	hypothetical prote
51	78	6.5	471	2	B64099	stage III sporulat
52	78	6.5	1297	2	T39287	undecaprenyl-phosp
53	77.5	6.5	2136	2	A05037	hypothetical prote
54	77.5	6.5	269	2	AH1175	hypothetical purese
55	77.5	6.5	299	2	AE0461	spermidine/putresc
56	77.5	6.5	327	2	F82904	probable membrane
57	77.5	6.5	328	2	F84130	conserved hypothet
58	77.5	6.5	440	2	T39159	hypothetical prote
59	77.5	6.5	491	2	T11319	A10L protein - var
60	77.5	6.5	491	2	B69499	NADH2 dehydrogenas
61	77.5	6.5	512	2	AC3399	sodium- and chlori
62	77.5	6.5	734	1	DERZN5	probable colanic b
63	77.5	6.5	892	2	T28552	NADH2 dehydrogenas
64	77.5	6.5	892	2	B36849	A1lL protein - var
65	77.5	6.5	892	2	T43167	hypothetical prote
66	77.5	6.5	1784	2	T23307	NADH2 dehydrogenas
67	77	6.4	332	2	C87307	hypothetical trans
68	77	6.4	559	2	QQUTC5	probable secretion
69	77	6.4	550	1	A90072	probable iron-upta
70	77	6.4	991	2	T01377	potassium channel
71	77	6.4	1025	2	T18376	probable membrane
72	77	6.4	1117	2	C85018	hypothetical prote
73	77	6.4	1500	2	G84922	potassium channel
74	76.5	6.4	278	2	B85807	probable voltage-d
75	76.5	6.4	278	2	H90958	protein C48A7.1 [i
76	76.5	6.4	282	2	H72164	melatonin receptor
77	76.5	6.4	352	2	T24664	hypothetical prote
78	76.5	6.4	352	2	T25170	hypothetical prote
79	76.5	6.4	352	2	AF0692	conserved hypothet
80	76.5	6.4	494	2	JC5919	hypothetical prote
81	76.5	6.4	538	2	E81435	NADH2 dehydrogenas
82	76.5	6.4	589	2	A71918	hypothetical prote
83	76.5	6.4	646	2	T41545	hypothetical tail fibe
84	76	6.4	342	2	T11476	phage tail protein
85	76	6.4	402	2	T24184	probable sugar ABC
86	76	6.4	669	2	T48466	hypothetical prote
87	76	6.4	1402	2	JC6139	cystic fibrosis tr
88	76	6.4	1450	2	T37258	probable voltage-d
89	76	6.4	1783	2	C88728	hypothetical prote
90	76	6.4	1917	2	I62107	hypothetical prote
91	75.5	6.3	156	2	G95198	melatonin receptor
92	75.5	6.3	263	2	C98065	hypothetical prote
93	75.5	6.3	263	2	E82211	hypothetical prote
94	75.5	6.3	263	2	H64919	conserved hypothet
95	75.5	6.3	352	2	G85769	hypothetical prote
96	75.5	6.3	352	2	C90921	probable membrane
97	75.5	6.3	352	2	F91209	hypothetical prote
98	75.5	6.3	415	2	A86056	low affinity trypt
99	75.5	6.3	415	2	A39412	low affinity trypt
100	75.5	6.3	415	2	S40689	tryptophan transpo
101	75.5	6.3	471	2	T11039	5-hydroxytryptamin
102	75.5	6.3	498	2	T11039	NADH2 dehydrogenas

#	%			len		Accession	Description
103	75.5	2	6.3	593	2	H64594	multidrug resistan
104	75.5	2	6.3	708	2	T29669	hypothetical prote
105	75.5	2	6.3	775	2	T52107	anion channel prot
106	75.5	1	6.3	1142	2	T39103	probable negative
107	75	2	6.3	249	2	G64470	sulfate/thiosulfat
108	75	2	6.3	274	2	A82509	probable phosphati
109	75	2	6.3	330	2	B71163	probable oligopept
110	75	2	6.3	473	2	A38627	gamma-aminobutyric
111	75	2	6.3	526	2	T45850	hypothetical prote
112	75	2	6.3	649	2	C69810	anion-binding prot
113	75	2	6.3	753	2	H90124	hypothetical prot
114	75	1	6.3	2248	2	D42088	adenylate cyclase
115	75	2	6.2	276	2	A95881	probable trehalose
116	74.5	2	6.2	335	2	H72420	oligopeptide ABC t
117	74.5	2	6.2	355	2	JC4304	orphan G protein-c
118	74.5	2	6.2	471	2	A34863	serotonin receptor
119	74.5	2	6.2	473	2	B84143	Na+/H+ antiporter
120	74.5	2	6.2	500	1	T14826	transcription init
121	74.5	2	6.2	574	2	T05964	probable low-affin
122	74.5	1	6.2	618	1	S38004	probable transport
123	74.5	1	6.2	1808	1	T47792	hypothetical prote
124	74	2	6.2	231	1	JC6311	cobalamin (5'-phos
125	74	2	6.2	231	2	B69422	quinone-reactive N
126	74	2	6.2	281	1	S26018	NADH2 dehydrogenas
127	74	2	6.2	286	2	S73424	spermidine/putresc
128	74	2	6.2	312	2	C72547	probable aspartate
129	74	2	6.2	312	2	H86732	hypothetical prote
130	74	2	6.2	349	1	JC6311	interferon recepto
131	74	2	6.2	350	2	I38848	Mel-1a melatonin r
132	74	2	6.2	396	2	H89869	hypothetical prote
133	74	2	6.2	442	2	C86859	transmembrane effl
134	74	2	6.2	449	2	S02011	serotonin receptor
135	74	2	6.2	475	2	T36137	probable amino aci
136	74	2	6.2	485	1	T24115	hypothetical prote
137	74	2	6.2	487	2	S76713	cytochrome P450 d1
138	74	2	6.2	493	2	C71417	L-lysine 6-aminotr
139	74	1	6.2	1123	2	JC7378	telomerase reverse
140	73.5	2	6.2	153	2	T51517	conserved hypothet
141	73.5	2	6.2	192	2	E95845	hypothetical prote
142	73.5	2	6.2	216	2	A84727	hypothetical prote
143	73.5	2	6.2	318	2	G70474	hypothetical prote
144	73.5	2	6.2	338	1	I40448	conserved hypothet
145	73.5	2	6.2	379	2	S58448	ubiquinol-cytochro
146	73.5	2	6.2	384	2	AF0636	glucans biosynthes
147	73.5	1	6.2	385	1	S01511	ubiquinol-cytochro
148	73.5	2	6.2	385	2	A69804	RNA-directed RNA p
149	73.5	2	6.2	413	2	AD1738	ABC transporter (A
150	73.5	2	6.2	442	2	C96672	Similar to multidr
151	73.5	2	6.2	491	1	EDBEM5	hypothetical prote
152	73.5	2	6.2	634	2	F82623	immediate-early pr
153	73.5	2	6.2	637	2	H83945	potassium uptake p
154	73.5	2	6.2	640	2	B32935	DNA mismatch repai
155	73.5	2	6.2	731	2	T31914	hypothetical prote
156	73.5	2	6.2	731	2	E96744	probable oligopept
157	73.5	2	6.2	1095	2	A39927	RNA-directed RNA p
158	73.5	1	6.2	1174	2	P71925	cag island protein
159	73	2	6.1	114	2	S26030	NADH2 dehydrogenas
160	73	2	6.1	282	2	T15560	hypothetical prote
161	73	1	6.1	339	1	WZBEE4	49.2K membrane pro
162	73	2	6.1	450	2	T30985	hypothetical prote
163	73	2	6.1	453	2	A71823	hypothetical prote
164	73	2	6.1	553	2	G89901	hypothetical prote
165	73	2	6.1	788	2	T00268	hypothetical prote
166	73	2	6.1	971	2	B96508	hypothetical prote
167	73	1	6.1	1075	2	S20901	titin - rabbit (fr
168	72.5	2	6.1	6805	2	S72929	hypothetical prote
169	72.5	2	6.1	209	2	B85866	probable transport
170	72.5	2	6.1	222	2	B91022	probable transport
171	72.5	2	6.1	222	2	H64996	hypothetical prote
172	72.5	2	6.1	222	2	A60944	ubiquinol-cytochro
173	72.5	2	6.1	255	2	T02986	chlorophyll a/b-bi
174	72.5	2	6.1	291	2	A86696	conserved hypothet
175	72.5	2	6.1	307	2	H96598	protein F20N2.8 [i
176	72.5	2	6.1	325	2	H86670	hypothetical prote
177	72.5	2	6.1	336	2	C89951	protein C38C3.2 [i
178	72.5	2	6.1	389	2	A55493	oxytocin receptor
179	72.5	2	6.1	428	2	AF0173	probable paraquat-
180	72.5	2	6.1	499	2	H70453	virulence factor M
181	72.5	1	6.1	513	2	S47631	pituitary adenylat
182	72.5	2	6.1	522	2	T29705	hypothetical prote
183	72.5	2	6.1	635	2	T23465	hypothetical prote
184	72.5	2	6.1	718	2	S57913	probable transloca
185	72	2	6.1	749	2	C84508	probable cap-bindi
186	72	1	6.1	1539	2	T30037	hypothetical prote
187	72	2	6.1	279	2	T21099	hypothetical prote
188	72	2	6.0	306	2	AE1196	hypothetical prote
189	72	2	6.0	339	2	G97199	probable permease
190	72	2	6.0	377	2	T27805	hypothetical prote
191	72	1	6.0	379	2	T11349	ubiquinol-cytochro
192	72	2	6.0	415	2	WMAD52	late L1 52K protei
193	72	2	6.0	415	1	WMAD65	late L1 52K protei
194	72	2	6.0	453	2	T31155	glycosyl hydrolase
195	72	2	6.0	453	2	D89760	conserved hypothet
196	72	2	6.0	479	2	S64587	hypothetical prote
197	72	2	6.0	479	2	G96611	probable cytochrom
198	72	2	6.0	497	2	T15338	probable cytochrom
199	72	2	6.0	514	2	T42660	hypothetical prote
200	72	2	6.0	594	2	T39873	hypothetical prote
201	72	2	6.0	600	2	T07966	probable ethylene
202	72	2	6.0	630	1	S37854	hypothetical prote
203	72	2	6.0	1038	2	S51280	DNA-directed DNA p
204	72	2	6.0	1094	2	T20140	hypothetical prote
205	72	2	6.0	1113	2	I46469	patched protein -
206	72	2	6.0	1220	2	T18291	trp protein - frui
207	72	2	6.0	1275	2	JU0092	P-glycoprotein 6 -
208	72	2	6.0	1282	2	T30804	cytochrome-c oxida
209	71.5	2	6.0	210	2	S52050	E1 membrane glycop
210	71.5	2	6.0	221	2	MMIH68	hypothetical prote
211	71.5	2	6.0	225	2	H79075	flagellar biosynth
212	71.5	2	6.0	237	2	AG3644	hypothetical prote
213	71.5	2	6.0	246	2	F86647	hypothetical prote
214	71.5	2	6.0	301	2	F90084	hypothetical prote
215	71.5	2	6.0	341	2	T33706	RhlD-related prote
216	71.5	2	6.0	345	2	D82252	sensory transducti
217	71.5	2	6.0	348	2	AB3516	prostaglandin E(2)
218	71.5	2	6.0	355	2	S48689	EP3-alpha receptor
219	71.5	2	6.0	362	2	S51280	Mel-1a melatonin r
220	71.5	2	6.0	366	2	T11776	ubiquinol-cytochro
221	71.5	2	6.0	366	2	T81194	hypothetical prote
222	71.5	2	6.0	381	2	S34043	oxytocin receptor
223	71.5	2	6.0	383	2	S66497	hypothetical prote
224	71.5	2	6.0	386	2	A49580	ubiquinol-cytochro
225	71.5	2	6.0	390	2	AB1340	isotocin receptor
226	71.5	2	6.0	435	2	AB1711	maltodextrin ABC-t
227	71.5	2	6.0	435	1	PS0154	maltodextrin ABC-t
228	71.5	2	6.0	471	2	T10124	125K surface antig
229	71.5	2	6.0	510	2	T02499	hexose transport p
230	71.5	2	6.0	524	2	H90061	hypothetical prote
231	71.5	2	6.0	603	2	T40050	betT protein homol
232	71.5	2	6.0	651	2	D64137	mediates transport
233	71.5	2	6.0	669	2	A49580	hypothetical prote
234	71.5	2	6.0	670	2	D64137	adenylate cyclase
235	71.5	2	6.0	823	2	S18030	genome polyprotein
236	71.5	1	6.0	3010	1	H64586	cag pathogenicity
237	71	2	5.9	1407	2	B42239	conserved hypothet
238	71	2	5.9	114	2	H64586	E1 membrane glycop
239	71	2	5.9	225	2	MMIHAI	chlorophyll a/b-bi
240	71	2	5.9	250	2	A82367	hypothetical prote
241	71	2	5.9	258	2	A81355	NADH2 dehydrogenas
242	71	2	5.9	290	2	S33443	probable processin
243	71	2	5.9	339	2	T16745	probable transport
244	71	2	5.9	345	2	T25561	hypothetical prote
245	71	2	5.9	345	2	T25372	hypothetical prote
246	71	2	5.9	361	2	C90603	3-deoxy-D-manno-oc
247	71	2	5.9	391	2	F87759	transcription regu
248	71	2	5.9	416	2	A43956	serotonin receptor

No.			Length		Accession	Description
249	71	5.9	546	2	S48932	hypothetical prote
250	71	5.9	563	2	T38766	probable transcrip
251	71	5.9	576	2	T22509	hypothetical prote
252	71	5.9	620	2	A58932	cytochrome C-type
253	71	5.9	676	2	E96725	hypothetical prote
254	71	5.9	788	2	E71813	probable component
255	71	5.9	913	2	T52485	neurofilament prot
256	71	5.9	2437	2	T18482	hypothetical prote
257	70.5	5.9	203	1	T31684	probable bacitraci
258	70.5	5.9	266	2	H98208	probable permease
259	70.5	5.9	266	2	AI3077	hypothetical prote
260	70.5	5.9	266	2	T41414	probable receptor-
261	70.5	5.9	279	2	AH2408	permease protein o
262	70.5	5.9	291	2	S22041	hypothetical prote
263	70.5	5.9	340	2	S76294	hypothetical prote
264	70.5	5.9	352	2	B90537	hypothetical prote
265	70.5	5.9	365	2	I38748	prostaglandin recep
266	70.5	5.9	365	2	S51315	hypothetical prote
267	70.5	5.9	374	2	I38747	prostaglandin E re
268	70.5	5.9	374	2	S51317	prostaglandin E re
269	70.5	5.9	388	2	S51316	prostaglandin E re
270	70.5	5.9	388	2	I38750	prostaglandin recep
271	70.5	5.9	389	2	S71336	mesotocin receptor
272	70.5	5.9	390	2	S43375	mesotocin receptor
273	70.5	5.9	390	2	S51313	prostaglandin E re
274	70.5	5.9	393	2	S51318	prostaglandin E re
275	70.5	5.9	423	1	E71065	hypothetical prote
276	70.5	5.9	425	2	S51319	prostaglandin E re
277	70.5	5.9	472	2	AG3600	cellulose synthase
278	70.5	5.9	496	2	B64638	conserved hypothet
279	70.5	5.9	521	2	B64181	probable cytochrom
280	70.5	5.9	548	2	A81650	hypothetical prote
281	70.5	5.9	556	2	T16790	probable membrane
282	70.5	5.9	574	2	S45754	gamma-aminobutyric
283	70.5	5.9	598	2	F46027	hypothetical prote
284	70.5	5.9	599	1	ACRTGT	gamma-aminobutyric
285	70.5	5.9	700	2	T10566	probable serine/th
286	70.5	5.9	766	2	T48463	hypothetical prote
287	70.5	5.9	1026	2	T18220	chitin synthase (E
288	70.5	5.9	1583	2	F97846	hypothetical prote
289	70.5	5.9	1787	2	T20160	hypothetical prote
290	70.5	5.9	5138	2	B96695	manganese-binding
291	70	5.9	189	2	T51847	manganese-binding
292	70	5.9	199	2	T08902	protein F1L3.8 (im
293	70	5.9	213	2	P86310	hypothetical prote
294	70	5.9	256	2	T11597	chlorophyll a/b-bi
295	70	5.9	287	2	T52317	H+-transporting tw
296	70	5.9	292	2	H64244	ABC transporter, P
297	70	5.9	307	2	E95010	hypothetical prote
298	70	5.9	307	2	B97882	hypothetical prote
299	70	5.9	330	2	T30981	hypothetical prote
300	70	5.9	333	2	I38974	G protein-coupled
301	70	5.9	371	2	T46421	oxytocin receptor
302	70	5.9	388	2	A55597	probable ankyrin-r
303	70	5.9	416	2	A85112	proline/betaine tr
304	70	5.9	418	2	T08882	sugar ABC transpor
305	70	5.9	420	2	E72357	hypothetical prote
306	70	5.9	427	2	T01105	hypothetical prote
307	70	5.9	437	2	C91261	glutamate-aspartat
308	70	5.9	437	2	G86101	glutamate-aspartat
309	70	5.9	438	2	AF3215	ABC transporter, m
310	70	5.9	450	2	T42595	envelope protein 5
311	70	5.9	494	2	B89827	hypothetical prote
312	70	5.9	532	2	T49467	related to COP1-in
313	70	5.9	551	2	A87019	probable cytochrom
314	70	5.9	554	2	T27878	hypothetical prote
315	70	5.9	558	2	H72565	hypothetical prote
316	70	5.9	675	2	T22323	hypothetical prote
317	70	5.9	735	2	S46830	urea transport pro
318	70	5.9	963	2	T26022	hypothetical prote
319	70	5.9	1930	2	F86200	protein F12K11.17
320	69.5	5.8	133	1	MNIHHC	nonstructural prot
321	69.5	5.8	206	2	S76279	hypothetical prote
322	69.5	5.8	285	2	F70194	hypothetical prote
323	69.5	5.8	321	2	S59388	probable membrane
324	69.5	5.8	339	2	A97736	hypothetical prote
325	69.5	5.8	347	2	G90444	hypothetical prote
326	69.5	5.8	354	2	A53216	probable G protein
327	69.5	5.8	361	2	S36764	prostaglandin E2 r
328	69.5	5.8	362	2	S36758	prostaglandin E re
329	69.5	5.8	384	2	S36766	ubiquinol-cytochro
330	69.5	5.8	385	2	S62758	prostaglandin E re
331	69.5	5.8	387	2	S36765	prostaglandin E re
332	69.5	5.8	394	2	S36767	hypothetical prote
333	69.5	5.8	400	2	T32561	cell-division prot
334	69.5	5.8	402	2	AG1208	Drosophila translo
335	69.5	5.8	405	2	S51791	Drosophila transla
336	69.5	5.8	405	2	H85831	probable colanic a
337	69.5	5.8	405	2	E90986	probable colanic a
338	69.5	5.8	405	2	G64971	Putative colanic a
339	69.5	5.8	417	2	S53216	prostaglandin E2 r
340	69.5	5.8	421	2	S36764	prostaglandin E re
341	69.5	5.8	436	2	G72300	conserved hypothet
342	69.5	5.8	453	2	T44832	probable emulsan r
343	69.5	5.8	477	2	D98003	conserved hypothet
344	69.5	5.8	490	2	T25798	C4-dicarboxylate t
345	69	5.8	503	2	E82740	C4-dicarboxylate t
346	69	5.8	507	2	C86250	hypothetical prote
347	69	5.8	515	2	T50054	probable transport
348	69	5.8	547	2	B86534	ADP/ATP translocas
349	69	5.8	547	2	G86581	integral membrane
350	69	5.8	557	2	T72042	organic cation tra
351	69	5.8	570	2	A61788	integral membrane
352	69	5.8	579	2	D97337	ABC transporter AT
353	69	5.8	579	2	AG1412	hypothetical prote
354	69	5.8	599	2	S11073	DNA polymerase III
355	69	5.8	604	2	T31042	DNA polymerase III
356	69	5.8	607	2	B84525	gamma-aminobutyric
357	69	5.8	616	2	E84463	hypothetical prote
358	69	5.8	877	2	S58824	Mutator-like trans
359	69	5.8	881	2	S71363	Mutator-like trans
360	69	5.8	1704	2	A59188	probable membrane
361	69	5.8	1704	2	JT0382	probable membrane
362	69	5.8	1704	2	I46509	probable ATP-bindi
363	69	5.8	1778	2	T15789	ATP-binding casset
364	69	5.8	2629	2	E83941	apolipoprotein B-
365	69.5	5.8	7829	2	A96998	apolipoprotein B -
366	69	5.8	169	2	H96934	hypothetical prote
367	69	5.8	195	2	C64145	hypothetical prote
368	69	5.8	244	2	T07481	hypothetical prote
369	69	5.8	256	2	F83805	CDP-diglyceride sy
370	69	5.8	261	2	C71707	uncharacterized me
371	69	5.8	273	2	S72554	hypothetical prote
372	69	5.8	273	2	D96002	hypothetical prote
373	69	5.8	289	2	T32702	hypothetical prote
374	69	5.8	291	2	A99979	melatonin receptor
375	69	5.8	300	2	B69436	probable sugar upt
376	69	5.8	338	2	AH1514	probable integral
377	69	5.8	339	2	AD0273	LSU ribosomal prot
378	69	5.8	345	2	S58447	hypothetical prote
379	69	5.8	351	2	AI31175	hypothetical prote
380	69	5.8	379	2	D71424	ubiquinol-cytochro
381	69	5.8	382	2	I69644	probable integral
382	69	5.8	382	2	T11268	conserved hypothet
383	69	5.8	383	2	A42384	hypothetical prote
384	69	5.8	388	2	T19512	O-antigen polymera
385	69	5.8	436	2	S25821	NADH2 dehydrogenas
386	69	5.8	437	2	T33985	glutamate-aspartat
387	69	5.8	443	2	E96804	hypothetical prote
388	69	5.8	478	2	T33985	hypothetical prote
389	69	5.8	478	2	S25821	transposase - Baci
390	69	5.8	508	2	E96804	hypothetical prote
391	69	5.8	523	2	T11916	probable thioredox
392	69	5.8	540	2	E70784	NADH2 dehydrogenas
393	69	5.8	549	2	T24675	cytochrome b homol
394	69	5.8	579	2	A64100	inner membrane cop

ID			Len	N	Accession	Description
395	69	5.8	599	2	G90476	probable Na+/H+ an
396	69	5.8	600	2	T11889	NADH2 dehydrogenas
397	69	5.8	637	2	H96592	probable multispan
398	69	5.8	659	2	D84633	probable multispan
399	69	5.8	791	2	T12455	potassium channel
400	69	5.8	802	2	JH0595	hypothetical prote
401	69	5.8	863	2	H84990	hypothetical membr
402	69	5.8	933	2	AD3309	hypothetical prote
403	69	5.8	1058	2	T30580	P-type ATPase - sl
404	69	5.8	1344	2	T34188	myb-binding protei
405	69	5.8	1392	2	T01908	hypothetical protei
406	69	5.8	1515	2	T04204	hypothetical prote
407	69	5.8	3010	1	A45573	genome polyprotein
408	68.5	5.7	225	2	AE0371	probable carboxype
409	68.5	5.7	237	2	T25877	hypothetical prote
410	68.5	5.7	238	2	T04280	hypothetical prote
411	68.5	5.7	260	2	H75428	hypothetical prote
412	68.5	5.7	262	2	AG1830	hypothetical prote
413	68.5	5.7	265	2	AI3428	hypothetical prote
414	68.5	5.7	285	2	E86835	O-antigen export s
415	68.5	5.7	297	2	S74335	maltose ABC transp
416	68.5	5.7	304	2	AG3035	carbon dioxide con
417	68.5	5.7	304	2	D98250	hypothetical prote
418	68.5	5.7	343	2	AC2129	iron(III) dicitrat
419	68.5	5.7	359	2	B59105	probable sugar ABC
420	68.5	5.7	362	2	D72424	oligopeptide ABC t
421	68.5	5.7	377	1	JQ2337	omega-3 fatty acid
422	68.5	5.7	383	2	I53870	Edg-1 orphan recep
423	68.5	5.7	391	2	H81265	hypothetical prote
424	68.5	5.7	395	2	B83774	probable transmemb
425	68.5	5.7	395	2	A96189	hypothetical prote
426	68.5	5.7	395	2	AH3097	conserved hypothet
427	68.5	5.7	419	2	AG1660	multidrug resistan
428	68.5	5.7	420	2	I51666	Mel-1c receptor su
429	68.5	5.7	425	2	F97108	hypothetical glycosylt
430	68.5	5.7	430	2	S15308	hypothetical prote
431	68.5	5.7	431	2	H72247	preprotein translo
432	68.5	5.7	444	2	A48260	corticoliberin rec
433	68.5	5.7	445	2	E22845	hypothetical prote
434	68.5	5.7	479	2	T44326	hypothetical prote
435	68.5	5.7	480	2	B70446	hypothetical prote
436	68.5	5.7	488	2	T15941	hypothetical prote
437	68.5	5.7	492	2	G90574	hypothetical prote
438	68.5	5.7	502	2	S77331	NADH2 dehydrogenas
439	68.5	5.7	512	2	T00605	hypothetical prote
440	68.5	5.7	518	2	S50465	probable cytochrom
441	68.5	5.7	525	2	JN0902	PAC2 protein - yea
442	68.5	5.7	542	2	S58102	pituitary adenylat
443	68.5	5.7	558	2	F64235	hypothetical prote
444	68.5	5.7	634	2	C83530	Na+ ATPase chain J
445	68.5	5.7	670	2	G86702	potassium uptake p
446	68.5	5.7	724	2	H86427	unknown protein [i
447	68.5	5.7	788	2	G64707	cation-transportin
448	68.5	5.7	923	1	MMBY7C	probable membrane
449	68.5	5.7	1004	1	S55353	probable copper-tr
450	68.5	5.7	146	2	H75201	hypothetical prote
451	68.5	5.7	205	2	A64373	hypothetical prote
452	68.5	5.7	255	2	F39925	hypothetical prote
453	68.5	5.7	266	2	C95316	probable ABC trans
454	68.5	5.7	270	2	AE3627	maltose transport
455	68.5	5.7	279	2	AG2165	bicarbonate transp
456	68.5	5.7	294	2	T41953	G protein-coupled
457	68.5	5.7	294	2	AE0004	ribonuclease BN (E
458	68.5	5.7	313	2	B38888	COI intron 9 prote
459	68.5	5.7	355	2	A45177	chemokine (C-C) re
460	68.5	5.7	360	2	T11067	ubiquinol-cytochro
461	68.5	5.7	364	2	JC2115	prostaglandin E re
462	68.5	5.7	365	2	JC2115	prostaglandin E2 r
463	68.5	5.7	370	2	H90559	hypothetical prote
464	68.5	5.7	379	2	AG0184	prostaglandin E r
465	68.5	5.7	393	2	A58450	ubiquinol-cytochro
466	68	5.7	402	2	T41253	probable multidrug
467	68	5.7	417	2	T11387	NADH2 dehydrogenas
468	68	5.7	426	2	C69831	conserved hypothet
469	68	5.7	464	2	C70414	NADH2 dehydrogenas
470	68	5.7	473	2	H71044	hypothetical prote
471	68	5.7	475	2	E83450	cytochrome-c oxida
472	68	5.7	477	2	H91123	cytochrome-c oxida
473	68	5.7	477	2	G85968	probable oxidoredu
474	68	5.7	477	2	G85096	probable oxidoredu
475	68	5.7	488	2	A53572	hypothetical 52.1
476	68	5.7	502	1	I30010	prostaglandin E2 r
477	68	5.7	519	2	T39918	prostaglandin
478	68	5.7	542	2	A69261	NADH2 dehydrogenas
479	68	5.7	542	2	B81910	NADH2 dehydrogenas
480	68	5.7	542	2	B81105	prostaglandin E2 r
481	68	5.7	620	2	T19907	hypothetical prote
482	68	5.7	664	2	C84869	probable receptor
483	68	5.7	718	2	B83718	hypothetical prote
484	68	5.7	804	2	T49975	probable acetyl-co
485	68	5.7	836	2	T18460	probable acid-CoA
486	68	5.7	859	2	S69700	probable ABC-trans
487	68	5.7	871	2	H72597	ABC transporter, A
488	68	5.7	1429	2	T19422	hypothetical prote
489	68	5.7	1878	2	E86189	hypothetical prote
490	68	5.7	3010	1	GNWVTC	genome polyprotein
491	67.5	5.6	104	2	T36801	hypothetical prote
492	67.5	5.6	200	2	H72295	conserved hypothet
493	67.5	5.6	273	2	A97700	conserved hypothet
494	67.5	5.6	288	2	F72219	hypothetical prote
495	67.5	5.6	320	2	T23674	conserved hypothet
496	67.5	5.6	323	2	QOBED3	HHRF3 protein - hu
497	67.5	5.6	348	2	T12591	NADH2 dehydrogenas
498	67.5	5.6	354	2	T09353	G protein-coupled
499	67.5	5.6	362	2	C88086	protein T11F1.1 [i
500	67.5	5.6	387	2	T24581	hypothetical prote
501	67.5	5.6	397	2	C88087	mutants block spor
502	67.5	5.6	419	2	B83999	multidrug resistan
503	67.5	5.6	439	2	AH1288	sodium-dependent c
504	67.5	5.6	450	2	H83699	hypothetical prote
505	67.5	5.6	450	2	H83699	hypothetical prote
506	67.5	5.6	450	2	A86066	hypothetical prote
507	67.5	5.6	452	2	F65183	4-alpha-1-fucosylt
508	67.5	5.6	459	2	G89870	TDP-Fuc4NAc lipid
509	67.5	5.6	483	2	JH0594	TDP-Fuc4NAc lipid
510	67.5	5.6	483	2	G84113	vasoactive intesti
511	67.5	5.6	492	1	QXASM4	NADH2 dehydrogenas
512	67.5	5.6	498	2	F64464	sodium-dependent n
513	67.5	5.6	516	2	T48262	hypothetical prote
514	67.5	5.6	516	2	E72089	ADP, ATP carrier p
515	67.5	5.6	598	2	H82973	choline transporte
516	67.5	5.6	632	2	I51368	gamma-aminobutyric
517	67.5	5.6	676	1	A71259	probable dicarboxy
518	67.5	5.6	676	2	W2VZ18	I8 protein - vacci
519	67.5	5.6	676	2	G91219	NPH-II, helicase -
520	67.5	5.6	676	2	T37345	I8R protein - vacc
521	67.5	5.6	676	2	P36843	ATP/GTP-binding pr
522	67.5	5.6	682	2	T28500	hypothetical prote
523	67.5	5.6	686	2	D72158	L8R protein - vari
524	67.5	5.6	716	2	G82448	sensor histidine k
525	67.5	5.6	740	1	S30687	hypothetical prote
526	67.5	5.6	838	2	A54163	probable ATP-bindi
527	67.5	5.6	866	2	T20574	vacuolar ATPase (E
528	67.5	5.6	950	2	T15915	hypothetical prote
529	67.5	5.6	1159	2	T02866	hypothetical prote
530	67.5	5.6	1244	2	T19615	hypothetical prote
531	67.5	5.6	1411	2	T02567	PDR11 protein - ye
532	67.5	5.6	1753	2	S48442	hypothetical prote
533	67.5	5.6	2332	1	S30855	genome polyprotein
534	67	5.6	151	2	A72093	conserved hypothet
535	67	5.6	151	2	T72093	CT101 hypothetical
536	67	5.6	159	2	H86529	probable membrane
537	67	5.6	159	2	S61040	Xe169 (escapes X-i
538	67	5.6	180	2	I48129	hypothetical prote
539	67	5.6	203	2	D70150	probable glycop
540	67	5.6	225	1	D70404	conserved hypothet

No.			Len		Code	Description
541	67	5.6	255	2	C90078	hypothetical prote
542	67	5.6	275	2	G98194	sugar ABC transpor
543	67	5.6	275	2	AC3092	hypothetical transpor
544	67	5.6	275	2	S75698	hypothetical prote
545	67	5.6	276	2	F69307	conserved hypothet
546	67	5.6	276	2	S35270	DNA-damage repair
547	67	5.6	283	2	F96959	tRNA-processing ri
548	67	5.6	285	2	AE3024	hypothetical prote
549	67	5.6	286	2	D64235	hypothetical prote
550	67	5.6	314	2	D96703	hypothetical prote
551	67	5.6	317	2	D98260	inner membrane pro
552	67	5.6	336	2	A96997	ferrichrome transp
553	67	5.6	345	2	T21776	hypothetical prote
554	67	5.6	349	2	D84166	hypothetical prote
555	67	5.6	350	2	C88987	protein C50H11.2 [
556	67	5.6	352	2	T32314	hypothetical prote
557	67	5.6	379	2	S58451	ubiquinol-cytochro
558	67	5.6	379	2	S58449	ubiquinol-cytochro
559	67	5.6	396	2	C69291	glucose transporte
560	67	5.6	407	2	E70309	hypothetical prote
561	67	5.6	411	2	B71500	probable amino aci
562	67	5.6	415	2	S74041	pyruvate synthase
563	67	5.6	416	2	T46401	hypothetical prote
564	67	5.6	423	2	AC1021	sodium-dependent t
565	67	5.6	436	2	C95085	proton glutamate s
566	67	5.6	441	2	F86279	hypothetical prote
567	67	5.6	446	2	G72287	hypothetical prote
568	67	5.6	496	2	A31986	glucose transporte
569	67	5.6	507	2	AB1707	glycine betaine tr
570	67	5.6	516	2	AE0665	probable membrane
571	67	5.6	646	2	JC7777	ATP binding casset
572	67	5.6	717	2	T49238	probable serine/th
573	67	5.6	753	2	S58331	dolichyl-phosphate
574	67	5.6	769	2	F81415	conserved hypothet
575	67	5.6	784	2	C82679	DNA topoisomerase
576	67	5.6	787	2	PN0677	probable NADH dehy
577	67	5.6	798	2	T34248	galactosamine-cont
578	67	5.6	814	2	T05537	chitin synthase (E
579	67	5.6	823	2	T35280	cell division prot
580	67	5.6	880	2	D69427	hypothetical prote
581	67	5.6	891	2	B82495	probable integral
582	67	5.6	900	2	E69631	hypothetical prote
583	67	5.6	1175	2	S39951	pleiotropic drug r
584	67	5.6	1242	1	DJBEC1	DNA-directed DNA p
585	67	5.6	1333	2	S63403	probable membrane
586	67	5.6	1511	2	A53151	conserved hypothet
587	67	5.6	1575	2	G82905	hypothetical prote
588	67	5.6	1879	2	T19481	multidrug resistan
589	67	5.6	1905	2	T18267	sodium channel SCA
590	67	5.6	1993	2	T30902	genome polyprotein
591	67	5.6	3010	1	GNWVCJ	conserved hypothet
592	66.5	5.6	153	1	G69847	hypothetical prote
593	66.5	5.6	203	2	T28732	sugar ABC transpor
594	66.5	5.6	204	2	C70506	ABC transporter, p
595	66.5	5.6	218	2	C64586	cag pathogenicity
596	66.5	5.6	245	2	A81405	sec-independent pr
597	66.5	5.6	263	2	AI2384	hypothetical prote
598	66.5	5.6	268	2	A70417	conserved hypothet
599	66.5	5.6	272	2	AI0075	hypothetical prote
600	66.5	5.6	279	2	S56642	probable permease
601	66.5	5.6	279	1	E70322	nitrate transport
602	66.5	5.6	293	2	A84110	hypothetical prote
603	66.5	5.6	294	2	S70876	sugar ABC transpor
604	66.5	5.6	316	2	F81712	hypothetical prote
605	66.5	5.6	333	2	S77103	hypothetical prote
606	66.5	5.6	347	2	AD2201	hypothetical prote
607	66.5	5.6	356	2	T20737	hypothetical prote
608	66.5	5.6	359	2	F90055	conserved hypothet
609	66.5	5.6	367	2	S75836	hypothetical prote
610	66.5	5.6	380	2	G89786	hypothetical prote
611	66.5	5.6	384	1	T38890	hypothetical prote
612	66.5	5.6	389	2	E96516	dual specificity p
613	66.5	5.6	400	2	G00013	F16N3.13 [imported
614	66.5	5.6	412	2	G89773	hypothetical prote
615	66.5	5.6	413	2	H95041	polysaccharide tra
616	66.5	5.6	435	2	D98111	hypothetical prote
617	66.5	5.6	435	2	G95246	maltodextrin ABC t
618	66.5	5.6	453	2	B95135	MATE efflux family
619	66.5	5.6	462	2	H71228	hypothetical prote
620	66.5	5.6	488	2	G71969	cytochrome-c oxida
621	66.5	5.6	490	2	D84998	low-affinity inorg
622	66.5	5.6	490	2	A46391	cAMP receptor subt
623	66.5	5.6	491	2	AC1555	efflux transporter
624	66.5	5.6	493	2	A71875	hypothetical prote
625	66.5	5.6	494	2	T32644	hypothetical prote
626	66.5	5.6	507	2	T27627	nickel transport s
627	66.5	5.6	539	2	G83720	probable alkaline
628	66.5	5.6	547	2	E91135	probable alkaline
629	66.5	5.6	547	2	H85980	sterol O-acyltrans
630	66.5	5.6	550	1	A48026	hypothetical prote
631	66.5	5.6	582	2	C71424	C-terminal domain
632	66.5	5.6	583	2	AI1510	hypothetical prote
633	66.5	5.6	598	2	T32430	cytochrome c-type
634	66.5	5.6	663	2	AG2696	cytochrome c-type
635	66.5	5.6	663	2	G97478	Na+/Cl(-)-dependen
636	66.5	5.6	727	2	I56506	Na+/Cl(-)-dependen
637	66.5	5.6	727	2	S27043	neurotransmitter t
638	66.5	5.6	782	2	S19876	genome polyprotein
639	66.5	5.6	862	2	B36786	hypothetical prote
640	66.5	5.6	889	2	T47311	hypothetical prote
641	66.5	5.6	992	2	T27479	hypothetical prote
642	66.5	5.6	1014	2	T31433	hypothetical prote
643	66.5	5.6	1083	2	C88854	protein F1A10.3 [
644	66.5	5.6	1144	2	H81037	DNA polymerase III
645	66.5	5.6	1456	2	T15961	hypothetical prote
646	66.5	5.6	1684	2	T15961	gravin - human
647	66.5	5.6	1684	2	JW0057	hypothetical prote
648	66.5	5.6	2151	2	GNWVC3	genome polyprotein
649	66.5	5.6	2285	1	A43360	diacylglycerol kin
650	66.5	5.6	2833	2	G02434	conserved hypothet
651	66.5	5.6	3011	1	S16449	hypothetical prote
652	66.5	5.6	93	1	S28759	genome polyprotein
653	66	5.5	130	2	D83820	hypothetical prote
654	66	5.5	209	2	A89801	conserved hypothet
655	66	5.5	276	2	H96816	hypothetical prote
656	66	5.5	279	2	S42125	sulfate ABC transp
657	66	5.5	285	2	D87447	hypothetical prote
658	66	5.5	302	2	A99074	hypothetical prote
659	66	5.5	305	2	I47040	hypothetical prote
660	66	5.5	305	2	B84671	sterol O-acyltrans
661	66	5.5	318	2	B84291	iron transport pro
662	66	5.5	322	2	E71137	hypothetical prote
663	66	5.5	332	2	C97272	hypothetical prote
664	66	5.5	370	1	I52315	conserved membrane
665	66	5.5	379	1	S17405	G protein-coupled
666	66	5.5	379	2	S17409	ubiquinol-cytochro
667	66	5.5	379	2	S58460	ubiquinol-cytochro
668	66	5.5	381	2	Q35300	G protein-coupled
669	66	5.5	390	2	QOBET9	protein UI33 - hum
670	66	5.5	390	2	T21154	protein UI33 - hum
671	66	5.5	397	2	T44477	hypothetical prote
672	66	5.5	397	2	B70505	hypothetical prote
673	66	5.5	401	2	T44831	probable emulsan r
674	66	5.5	404	1	B64927	probable sugar tra
675	66	5.5	404	2	A85777	probable sugar tra
676	66	5.5	404	2	E90928	probable transport
677	66	5.5	411	2	H86539	CBS domain protein
678	66	5.5	412	2	A82444	GGDEF family prote
679	66	5.5	418	2	T41027	hypothetical wtf5
680	66	5.5	418	2	B72353	hypothetical prote
681	66	5.5	424	2	T07366	probable phosphati
682	66	5.5	436	2	T14816	probable phosphati
683	66	5.5	447	2	T18633	hypothetical prote
684	66	5.5	450	2	A37223	alpha-2B-adrenergi
685	66	5.5	450	2	A38316	alpha-2-adrenergic
686	66	5.5	453	2	F86846	ABC transporter pe

No.			Len	N	Accession	Description
687	66	5.5	483	2	S75369	hypothetical prote
688	66	5.5	484	2	T24238	hypothetical prote
689	66	5.5	496	2	E82940	hypothetical prote
690	66	5.5	508	2	G47677	hypothetical prote
691	66	5.5	525	2	T28306	ORF MSV145 hypothe
692	66	5.5	527	2	G69635	PTS arbutin-like e
693	66	5.5	532	2	A90037	hypothetical prote
694	66	5.5	546	2	A69890	hypothetical prote
695	66	5.5	548	2	B87423	cytochrome-c oxida
696	66	5.5	552	2	S45886	hypothetical prote
697	66	5.5	565	2	S73707	Na(+) translocatin
698	66	5.5	570	2	S07744	NADH2 dehydrogenas
699	66	5.5	573	1	S33212	INDA1 protein - fu
700	66	5.5	573	2	AF1418	ABC transporter, A
701	66	5.5	573	2	AH1793	ABC transporter, A
702	66	5.5	619	2	T11314	NADH2 dehydrogenas
703	66	5.5	632	2	T24405	hypothetical prote
704	66	5.5	654	2	A98350	hypothetical ABC t
705	66	5.5	654	2	AF2932	hypothetical prote
706	66	5.5	705	2	T48464	hypothetical prote
707	66	5.5	721	2	A70764	hypothetical prote
708	66	5.5	736	2	G01522	probable glgX prot
709	66	5.5	784	2	B90442	acidic 82 kDa prot
710	66	5.5	1039	2	S76747	titin, cardiac mus
711	66	5.5	1054	2	A61221	tricorn proteinase
712	66	5.5	1359	2	T34036	hypothetical prote
713	66	5.5	1375	2	S48375	hypothetical prote
714	66	5.5	1581	2	P90608	ABC transporter Pe
715	66	5.5	2599	1	S67771	endoplasmic reticu
716	66	5.5	26926	1	I38344	titin, cardiac mus
717	65.5		132	2	E97760	NADH2 dehydrogenas
718	65.5		132	2	E70074	hypothetical prote
719	65.5		146	2	G69447	hypothetical prote
720	65.5		171	2	AI3476	signal peptidase I
721	65.5		197	2	T17106	polysulfide reduct
722	65.5		210	2	S23459	probable binding p
723	65.5		252	2	T36087	hypothetical prote
724	65.5		290	2	S36003	NADH2 dehydrogenas
725	65.5		297	1	AH0362	nucleoside permeas
726	65.5		297	2	T11064	hypothetical prote
727	65.5		301	2	T32601	NADH2 dehydrogenas
728	65.5		317	2	T32778	hypothetical prote
729	65.5		327	2	S58456	hypothetical prote
730	65.5		348	1	JC2056	ubiquinol-cytochro
731	65.5		351	1	F69629	spore germination
732	65.5		365	1	P82880	hypothetical ferri
733	65.5		367	2	F69456	hypothetical prote
734	65.5		379	2	T43100	hypothetical prote
735	65.5		379	2	S67771	NADH2 dehydrogenas
736	65.5		391	2	T21308	hypothetical prote
737	65.5		394	2	E83792	conserved hypothet
738	65.5		410	2	F86839	conserved hypothet
739	65.5		423	2	E90569	hypothetical prote
740	65.5		425	2	T38916	probable transcrip
741	65.5		425	2	AF2913	microfibril-associ
742	65.5		429	2	A42670	probable dicarboxy
743	65.5		442	2	T32832	hypothetical prote
744	65.5		445	2	H83629	hypothetical prote
745	65.5		449	2	A75327	hypothetical prote
746	65.5		457	2	B75170	endoplasmic reticu
747	65.5		477	2	A60043	type I site-specif
748	65.5	1	480	2	H64537	cytochrome-c oxida
749	65.5		487	2	A97928	cytochrome-c oxida
750	65.5		488	2	G81295	efflux transporter
751	65.5		491	2	AE1197	probably membrane
752	65.5		495	2	A97022	hypothetical prote
753	65.5		500	2	G84706	NADH2 dehydrogenas
754	65.5		502	2	AD3395	hypothetical prote
755	65.5		502	2	A53207	hypothetical prote
756	65.5		518	2	T25669	probable folate tr
757	65.5		528	2	T34417	delayed rectifier
758	65.5		544	2	B84825	probable ABC trans
759	65.5		545	2	E90460	hypothetical prote

No.			Len	N	Accession	Description
760	65.5	5.5	561	2	S71189	Dwarf1 protein - A
761	65.5	5.5	575	2	AH1417	ABC transporter (A
762	65.5	5.5	578	2	T15736	hypothetical prote
763	65.5	5.5	583	2	AH1151	glycerophosphoryl
764	65.5	5.5	590	2	C81316	hypothetical sugar epi
765	65.5	5.5	597	2	B82881	hypothetical prote
766	65.5	5.5	617	2	AB1167	phosphotransferase
767	65.5	5.5	618	2	AC1204	phosphotransferase
768	65.5	5.5	642	2	H70331	ATP-dependent heli
769	65.5	5.5	718	2	H92198	Na+/myo-inositol c
770	65.5	5.5	720	2	AF1254	RTX toxin transpor
771	65.5	5.5	721	2	S61568	penicillin-binding
772	65.5	5.5	740	1	QRHLD	probable membrane
773	65.5	5.5	860	1	AC0204	LDL receptor precu
774	65.5	5.5	958	2	S41797	probable integral
775	65.5	5.5	1087	2	B22999	cellulose 1,4-beta
776	65.5	5.5	1328	2	S74293	TyB protein - yea
777	65.5	5.5	1427	2	B75099	SRB8 protein - yea
778	65.5	5.5	1581	2	B71636	hypothetical prote
779	65.5	5.5	1635	2	T32452	hypothetical prote
780	65.5	5.4	126	2	AD0340	probable membrane
781	65.5	5.4	149	2	G15293	transcription regu
782	65.5	5.4	176	1	Q1AD25	early E1B 21K prot
783	65.5	5.4	196	2	S75957	hemA concentration
784	65.5	5.4	225	1	T02877	nitrate transport
785	65.5	5.4	247	2	C97453	probable chlorophy
786	65.5	5.4	257	2	AE26711	dipeptide abc tran
787	65.5	5.4	259	2	AD1200	NADH2 dehydrogenas
788	65.5	5.4	271	2	B36125	hypothetical prote
789	65.5	5.4	280	2	A64084	conserved hypothet
790	65.5	5.4	290	2	D87087	branched-chain ami
791	65.5	5.4	291	2	S38091	cytochrome c oxida
792	65.5	5.4	291	2	H69785	cytochrome-c oxida
793	65.5	5.4	291	1	I38879	serotonin receptor
794	65.5	5.4	307	2	MMHIV	E1 membrane glycop
795	65.5	5.4	313	2	I48149	hypothetical prote
796	65.5	5.4	319	2	A47112	lysophospholipase
797	65.5	5.4	322	2	B75099	hypothetical prote
798	65.5	5.4	330	2	A64084	growth response pr
799	65.5	5.4	335	1	E89950	hypothetical prote
800	65.5	5.4	338	2	S38091	hypothetical prote
801	65.5	5.4	344	1	H69785	mannan endo-1,4-be
802	65.5	5.4	345	2	I38879	corticotropin rele
803	65.5	5.4	355	1	S17414	ubiquinol-cytochro
804	65.5	5.4	359	1	S58451	ubiquinol-cytochro
805	65.5	5.4	359	2	S58455	ubiquinol-cytochro
806	65.5	5.4	362	2	S50339	ubiquinol-cytochro
807	65.5	5.4	375	2	H75029	hypothetical prote
808	65.5	5.4	375	2	H75068	NADH2 dehydrogenas
809	65.5	5.4	379	1	H75029	conserved hypothet
810	65.5	5.4	379	2	D34285	hypothetical prote
811	65.5	5.4	380	2	T11138	NADH2 dehydrogenas
812	65.5	5.4	382	2	C84984	hypothetical prote
813	65.5	5.4	390	2	T21532	hypothetical prote
814	65.5	5.4	415	2	B81410	TRK system potassi
815	65.5	5.4	438	2	A83122	probable membrane
816	65.5	5.4	442	2	AD2358	protein T27E9.5 [I
817	65.5	5.4	445	2	T28334	Ser/Thr protein ki
818	65.5	5.4	457	2	B88613	glucosyltransferas
819	65.5	5.4	462	2	S54508	probable MFS trans
820	65.5	5.4	477	2	A69036	probable integral
821	65.5	5.4	479	2	E81050	hypothetical prote
822	65.5	5.4	481	2	T14545	hypothetical prote
823	65.5	5.4	490	2	S59107	probable sugar tra
824	65.5	5.4	490	2	S55204	cytochrome-c oxida
825	65.5	5.4	492	2	H75097	probable membrane
826	65.5	5.4	510	2	T37180	polysaccharide bio
827	65.5	5.4	511	2	D91047	probable membrane
828	65.5	5.4	513	2	B89771	hydrogenase 4 memb
829	65.5	5.4	526	2	A64697	hypothetical prote
830	65.5	5.4	530	2	S55190	conserved hypothet
831	65	5.4	535	2	S53920	SNG1 protein - yea
832	65	5.4	576	2	T25375	hypothetical prote

No.			Len	N	Accession	Description
833	65	5.4	579	2	S61131	probable membrane
834	65	5.4	608	2	S65298	dicarboxylic amino
835	65	5.4	611	2	T21747	hypothetical amino
836	65	5.4	624	2	G82508	hypothetical prote
837	65	5.4	627	2	T11125	NADH2 dehydrogenas
838	65	5.4	633	2	F84483	NADH2 dehydrogenas
839	65	5.4	638	2	D69957	Mutator-like trans
840	65	5.4	643	2	F97787	conserved hypothet
841	65	5.4	676	2	A45515	sodium/pantothenat
842	65	5.4	684	2	F86394	dnaK-type molecula
843	65	5.4	697	2	H84791	protein T24P13.20
844	65	5.4	702	2	T13505	hypothetical prote
845	65	5.4	705	2	T04400	NADH2 dehydrogenas
846	65	5.4	773	2	H96818	hypothetical prote
847	65	5.4	773	2	G83816	late competence op
848	65	5.4	808	2	T04459	hypothetical prote
849	65	5.4	861	2	S77086	hypothetical prote
850	65	5.4	927	2	T38518	ribonuclease II RN
851	65	5.4	931	2	F84637	probable plasma.me
852	65	5.4	938	2	T01809	hypothetical prote
853	65	5.4	1089	2	C70522	hypothetical prote
854	65	5.4	1163	2	D64315	probable mmpL8 pro
855	65	5.4	1178	2	S76370	type 1 restriction
856	65	5.4	1232	2	I38496	sensory transducti
857	65	5.4	1421	2	T34225	anion exchanger 3
858	65	5.4	5069	2	I17464	hypothetical prote
859	64.5	5.4	180	2	T41339	rifamycin polyketi
860	64.5	5.4	211	2	S35280	eaC protein - phag
861	64.5	5.4	217	2	AE0395	hypothetical prote
862	64.5	5.4	227	2	C69432	probable amino aci
863	64.5	5.4	234	2	E96957	probable amino
864	64.5	5.4	268	2	AF2470	HAD superfamily hy
865	64.5	5.4	271	2	E81384	hypothetical prote
866	64.5	5.4	275	2	T43119	prolipoprotein dia
867	64.5	5.4	293	2	D71517	hypothetical prote
868	64.5	5.4	297	2	T32202	probable metal tra
869	64.5	5.4	297	2	T27584	hypothetical prote
870	64.5	5.4	320	2	T23904	protein F3M18.6 [i
871	64.5	5.4	326	2	A86411	hypothetical prote
872	64.5	5.4	353	2	F64175	hypothetical prote
873	64.5	5.4	358	2	T22823	hypothetical prote
874	64.5	5.4	361	2	A86841	hypothetical prote
875	64.5	5.4	361	1	A40734	Pas (Passover) pro
876	64.5	5.4	379	2	S43264	ubiquinol-cytochro
877	64.5	5.4	379	2	T11505	ubiquinol-cytochro
878	64.5	5.4	379	2	S58454	ubiquinol-cytochro
879	64.5	5.4	379	2	A53077	ubiquinol-cytochro
880	64.5	5.4	381	1	CBMS	ubiquinol-cytochro
881	64.5	5.4	381	2	S33449	pituitary adenylat
882	64.5	5.4	385	2	H69154	hypothetical prote
883	64.5	5.4	398	2	H95057	phosphoglycerate k
884	64.5	5.4	398	1	A97927	phosphoglycerate k
885	64.5	5.4	400	2	G01977	d3 dopamine recept
886	64.5	5.4	411	2	S46800	LAG1 protein - yea
887	64.5	5.4	416	2	AF1127	rod shape-determin
888	64.5	5.4	426	2	T45800	UDP-N-acetylglucos
889	64.5	5.4	433	2	T11162	NADH2 dehydrogenas
890	64.5	5.4	435	2	AC0105	probable maltodext
891	64.5	5.4	439	2	C22845	NADH2 dehydrogenas
892	64.5	5.4	439	2	A84153	hypothetical prote
893	64.5	5.4	443	2	B26696	hypothetical prote
894	64.5	5.4	444	2	T11474	NADH2 dehydrogenas
895	64.5	5.4	444	2	A43676	P44 hepatitis-asso
896	64.5	5.4	444	2	S48218	microtubular aggre
897	64.5	5.4	446	1	DYRTD3	dopamine receptor
898	64.5	5.4	448	2	D85362	dopamine receptor
899	64.5	5.4	448	2	S57909	probable histidine
900	64.5	5.4	450	2	D70045	hypothetical prote
901	64.5	5.4	451	2	T23528	two-component sens
902	64.5	5.4	467	2	D70616	pituitary adenylat
903	64.5	5.4	478	2	C29051	transposase C - Ba
904	64.5	5.4	495	1	FWSYG2	glycinin chain Ala
905	64.5	5.4	495	2	S39061	pituitary adenylyl
906	64.5	5.4	495	2	S36114	pituitary adenylat
907	64.5	5.4	495	2	S10851	glycinin G1 precur
908	64.5	5.4	512	2	H64964	probable membrane
909	64.5	5.4	521	2	A99549	amino acid permeas
910	64.5	5.4	521	1	S39060	pituitary adenylyl
911	64.5	5.4	547	2	H65107	hypothetical prote
912	64.5	5.4	554	2	A56730	carl protein - Pod
913	64.5	5.4	554	2	B97812	virulence factor m
914	64.5	5.4	575	2	AB1793	ABC transporter (A
915	64.5	5.4	576	2	A81793	histidine kinase -
916	64.5	5.4	614	2	T05904	cytochrome P450 97
917	64.5	5.4	622	2	B89869	hypothetical prote
918	64.5	5.4	638	2	AC1236	acyltransferase (t
919	64.5	5.4	715	2	T26307	mRNA maturase bI4
920	64.5	5.4	720	1	T47648	hypothetical prote
921	64.5	5.4	721	2	AD1617	ABC transporter-li
922	64.5	5.4	721	2	AE1491	penicillin-binding
923	64.5	5.4	735	2	AD0341	hypothetical prote
924	64.5	5.4	763	2	AD1070	probable membrane
925	64.5	5.4	801	2	AD9862	phosphatidylglycer
926	64.5	5.4	803	2	H64568	Na+/H+ antiporter
927	64.5	5.4	889	2	T30715	histidine kinase -
928	64.5	5.4	979	2	A70848	probable major cor
929	64.5	5.4	1007	2	A70046	probable membrane
930	64.5	5.4	1114	2	JC8066	125K surface antig
931	64.5	5.4	1146	2	H70284	probable mmpL12 pr
932	64.5	5.4	1154	2	B70723	related to SREBP c
933	64.5	5.4	1465	2	T48829	DNA-directed DNA p
934	64.5	5.4	1529	2	S45628	hypothetical prote
935	64.5	5.4	1630	1	S69688	ESP1 protein - Yea
936	64.5	5.4	1661	2	S64800	probable membrane
937	64	5.4	202	1	GNWVJ8	genome polyprotein
938	64	5.4	209	2	A70041	conserved hypothet
939	64	5.4	253	2	G82359	cdd3 protein - Clo
940	64	5.4	259	2	C70040	conserved hypothet
941	64	5.4	269	2	T50567	hypothetical prote
942	64	5.4	270	2	F89632	protein F13E6.3 [i
943	64	5.4	274	2	H69768	probable ABC-type
944	64	5.4	276	2	T12451	plant-metabolite d
945	64	5.4	276	2	T12451	hypothetical prote
946	64	5.4	281	2	C95932	probable membrane
947	64	5.4	283	2	S48358	probable sugar upt
948	64	5.4	285	2	D83009	probable permease
949	64	5.4	288	2	B83883	sugar transport sy
950	64	5.4	330	2	S36955	cytochrome-c oxida
951	64	5.4	342	2	S36955	hypothetical prote
952	64	5.4	347	2	T29675	hypothetical prote
953	64	5.4	347	2	A48258	dopamine receptor
954	64	5.4	351	2	T11248	NADH2 dehydrogenas
955	64	5.4	351	2	S56716	protein kinase SPK
956	64	5.4	357	2	G01430	PL6 protein - huma
957	64	5.4	367	2	T20271	hypothetical prote
958	64	5.4	369	2	H90587	hypothetical prote
959	64	5.4	376	2	S26031	ubiquinol-cytochro
960	64	5.4	376	1	S26031	twitching motility
961	64	5.4	378	2	S43263	probable cytochrom
962	64	5.4	379	2	S17419	ubiquinol-cytochro
963	64	5.4	379	2	S25163	ubiquinol-cytochro
964	64	5.4	379	2	S43263	ubiquinol-cytochro
965	64	5.4	379	2	T11414	ubiquinol-cytochro
966	64	5.4	379	2	S58452	ubiquinol-cytochro
967	64	5.4	379	2	S58452	ubiquinol-cytochro
968	64	5.4	383	2	S55594	NA+/H+ antiporter
969	64	5.4	383	1	G64667	G protein-coupled
970	64	5.4	387	1	H71848	dopamine receptor
971	64	5.4	402	2	S74522	hypothetical prote
972	64	5.4	402	2	AD1417	hypothetical prote
973	64	5.4	404	2	A97559	drug-efflux transp
974	64	5.4	404	2	AE2779	acyltransferase [i
975	64	5.4	409	2	A55610	NADH2 dehydrogenas
976	64	5.4	411	2	S26021	corticotropin-rele
977	64	5.4	413	2	H81659	branched-chain ami
978	64	5.4	422	2	B84338	isocitrate dehydro

979	64	5.4	430	1	S32570	malc protein - Str
980	64	5.4	450	2	B40392	alpha-2-adrenergic
981	64	5.4	451	2	A36908	spore cortex penic
982	64	5.4	455	2	T31258	aromatic oxygenase
983	64	5.4	457	2	AF2975	aminotransferase,
984	64	5.4	457	2	E98307	probable aminotran
985	64	5.4	463	2	AC0281	probable amino aci
986	64	5.4	469	2	H90322	polysaccharide bio
987	64	5.4	492	2	E58931	NADH2 dehydrogenas
988	64	5.4	503	2	JC7627	cytochrome P450 3A
989	64	5.4	511	2	T40334	sodium- and chlori
990	64	5.4	527	2	A75122	hypothetical prote
991	64	5.4	536	2	T36109	hypothetical prote
992	64	5.4	538	2	C90406	conserved hypothet
993	64	5.4	544	2	T13877	NADH2 dehydrogenas
994	64	5.4	562	2	T52481	cytochrome-c oxida
995	64	5.4	575	2	G75282	probable glutathio
996	64	5.4	586	1	A34400	ezrin [validated]
997	64	5.4	598	2	T05130	hypothetical prote
998	64	5.4	602	2	C75120	hypothetical prote
999	64	5.4	606	2	B69805	conserved hypothet
1000	64	5.4	608	2	G02640	polycystic kidney
1001	64	5.4	609	2	F70512	protein -
1002	64	5.4	610	2	S37049	probable vacuolar
1003	64	5.4	614	2	A69845	F6A14.8 protein -
1004	64	5.4	630	2	T47177	H+-exporting ATPas
1005	64	5.4	654	2	C86677	Na+/H+ antiporter
1006	64	5.4	657	2	T52460	DNA ligase (NAD) (
1007	64	5.4	661	2	T51779	hypothetical prote
1008	64	5.4	674	2	T50347	non-phototropic hy
1009	64	5.4	696	2	AB1566	hypothetical prote
1010	64	5.4	748	2	T10651	hypothetical prote
1011	64	5.4	802	2	A87754	protein C43E11.11
1012	64	5.4	838	2	H82939	conserved hypothet
1013	64	5.4	860	2	T37768	hypothetical prote
1014	64	5.4	874	2	B86322	probable vacuolar
1015	64	5.4	896	2	AF1409	conserved hypothet
1016	64	5.4	991	2	S57385	the two components
1017	64	5.4	1024	2	RNZQBF	probable membrane
1018	64	5.4	1078	2	T19745	DNA-directed RNA p
1019	64	5.4	1081	2	B81303	hypothetical prote
1020	64	5.4	1227	2	A33638	probable membrane
1021	64	5.4	1385	2	T13415	erythrocyte anion
1022	64	5.4	1462	1	DJHUAC	hypothetical prote
1023	64	5.4	1695	2	JE0084	DNA-directed DNA p
1024	64	5.4	2496	2	A71616	voltage-gated sodi
1025	63.5	5.4	111	2	S43115	secreted protein P
1026	63.5	5.3	123	2	G71692	acidic ribosomal p
1027	63.5	5.3	147	2	AH0495	NADH2 dehydrogenas
1028	63.5	5.3	149	2	H70581	probable membrane
1029	63.5	5.3	195	2	E71000	hypothetical prote
1030	63.5	5.3	214	2	C90191	conserved hypothet
1031	63.5	5.3	218	2	B71925	hypothetical prote
1032	63.5	5.3	218	2	T29205	cag island protein
1033	63.5	5.3	231	2	F85679	hypothetical prote
1034	63.5	5.3	238	2	S75336	probable antiepre
1035	63.5	5.3	241	2	F86691	ABC transporter pe
1036	63.5	5.3	242	1	S74794	conserved hypothet
1037	63.5	5.3	246	2	AD3574	branched-chain ami
1038	63.5	5.3	259	2	AF0106	probable membrane
1039	63.5	5.3	275	2	E95161	hypothetical prote
1040	63.5	5.3	275	2	D98027	hypothetical prote
1041	63.5	5.3	275	2	G84320	hypothetical prote
1042	63.5	5.3	276	2	E96951	conserved membrane
1043	63.5	5.3	280	2	T16240	hypothetical prote
1044	63.5	5.3	282	2	E83086	conserved hypothet
1045	63.5	5.3	282	2	AB0346	hypothetical prote
1046	63.5	5.3	291	2	AB2939	probable ABC trans
1047	63.5	5.3	291	2	E98343	hypothetical prote
1048	63.5	5.3	291	2	F75571	hypothetical prote
1049	63.5	5.3	313	2	D26696	NADH2 dehydrogenas
1050	63.5	5.3	315	2	E69365	hypothetical prote
1051	63.5	5.3	316	2	H86665	ferrichrome ABC tr
1052	63.5	5.3	327	2	S56162	MDCR15 protein - h
1053	63.5	5.3	328	2	D98215	oligopeptide ABC t
1054	63.5	5.3	328	2	T39824	septin homolog - f
1055	63.5	5.3	334	2	B72393	oligopeptide ABC t
1056	63.5	5.3	334	2	T41037	hypothetical prote
1057	63.5	5.3	334	2	T27081	hypothetical prote
1058	63.5	5.3	342	2	A38908	spa40 protein - Sh
1059	63.5	5.3	344	2	T34981	probable integral
1060	63.5	5.3	355	2	T15203	hypothetical prote
1061	63.5	5.3	359	2	D90172	hypothetical prote
1062	63.5	5.3	361	2	AE3071	oligopeptide trans
1063	63.5	5.3	365	2	AB3494	hypothetical prote
1064	63.5	5.3	372	2	S26667	G protein-coupled
1065	63.5	5.3	372	2	B72275	probable aspartate
1066	63.5	5.3	380	1	CBRT	ubiquinol-cytochro
1067	63.5	5.3	381	2	T11312	ubiquinol-cytochro
1068	63.5	5.3	387	2	H88012	protein K10B4.2 [i
1069	63.5	5.3	389	2	G75133	hypothetical prote
1070	63.5	5.3	392	2	H71520	probable hth trans
1071	63.5	5.3	395	2	B81358	transmembrane tran
1072	63.5	5.3	398	2	C71682	ubiquinol-cytochro
1073	63.5	5.3	398	2	D81397	probable periplasm
1074	63.5	5.3	399	2	B95080	cell division prot
1075	63.5	5.3	400	2	AG3016	phosphoglycerate k
1076	63.5	5.3	400	1	T46306	ubiquinol-cytochro
1077	63.5	5.3	404	1	LABBCA	latent membrane pr
1078	63.5	5.3	404	2	T19887	hypothetical prote
1079	63.5	5.3	406	2	T04915	CDP-diacylglycerol
1080	63.5	5.3	423	2	G85255	CDP-diacylglycerol
1081	63.5	5.3	423	2	B81358	CDP-diacylglycerol
1082	63.5	5.3	426	2	A96268	phosphoglycerate k
1083	63.5	5.3	438	2	T33299	conserved hypothet
1084	63.5	5.3	444	2	A82262	hypothetical prote
1085	63.5	5.3	445	2	B85789	hypothetical prote
1086	63.5	5.3	447	2	T16025	CDP-diacylglycerol
1087	63.5	5.3	447	2	F90940	hypothetical prote
1088	63.5	5.3	450	2	S52437	CDP-diacylglycerol
1089	63.5	5.3	452	2	E96738	hypothetical prote
1090	63.5	5.3	461	2	T21118	sugar transferase
1091	63.5	5.3	468	2	C97187	hypothetical prote
1092	63.5	5.3	485	2	T46686	hypothetical prote
1093	63.5	5.3	485	2	H90562	mg2+ transport pro
1094	63.5	5.3	487	2	B55059	hypothetical prote
1095	63.5	5.3	491	2	A64939	hypothetical prote
1096	63.5	5.3	492	2	B90373	sugar transport re
1097	63.5	5.3	494	1	S76516	integral membrane
1098	63.5	5.3	498	2	T48385	transporter like p
1099	63.5	5.3	498	2	T16190	hypothetical prote
1100	63.5	5.3	500	2	AF2325	NADH dehydrogenase
1101	63.5	5.3	511	2	G90221	hypothetical prote
1102	63.5	5.3	512	2	A70201	virulence factor m
1103	63.5	5.3	525	2	A49601	nucleocapsid prote
1104	63.5	5.3	540	2	G82873	conserved hypothet
1105	63.5	5.3	540	1	149454	sterol O-acyltrans
1106	63.5	5.3	544	2	C96943	uncharacterized me
1107	63.5	5.3	551	2	E64537	L-lactate permease
1108	63.5	5.3	551	2	D71969	hypothetical prote
1109	63.5	5.3	555	2	G96744	probable peptide t
1110	63.5	5.3	567	2	C75340	probable L-lactate
1111	63.5	5.3	568	2	T17588	hyaluronoglucosami
1112	63.5	5.3	593	2	I46528	sodium/dicarboxyla
1113	63.5	5.3	594	2	E88956	protein ZK697.5 [i
1114	63.5	5.3	605	2	A36361	glucose transport
1115	63.5	5.3	605	2	H71562	probable flagellar
1116	63.5	5.3	605	2	T43974	hypothetical prote
1117	63.5	5.3	610	2	T44161	hypothetical prote
1118	63.5	5.3	668	2	B54759	ba-type ubiquinol
1119	63.5	5.3	671	2	B37237	probable kinase C (
1120	63.5	5.3	681	2	AF0697	protein kinase (
1121	63.5	5.3	683	2	A85044	probable type III
1122	63.5	5.3	708	2	JQ0148	hypothetical prote
1123	63.5	5.3	741	2	T20148	killer toxin KHS p
1124	63.5	5.3	780	2	T48189	NADH2 dehydrogenas
			787	2	A70132	cell division prot

No.			Len		Accession	Description
1125	63.5	5.3	819	2	T19351	hypothetical prote
1126	63.5	5.3	841	2	T38703	hypothetical prote
1127	63.5	5.3	843	2	T32487	hypothetical prote
1128	63.5	5.3	843	2	T41237	conserved hypoth
1129	63.5	5.3	844	2	AD2339	hypothetical prote
1130	63.5	5.3	951	2	T08987	probable cadmium-t
1131	63.5	5.3	966	2	H97717	hypothetical prote
1132	63.5	5.3	1004	2	G87323	hypothetical prote
1133	63.5	5.3	1098	2	S38100	hypothetical prote
1134	63.5	5.3	1229	2	S42391	SIP3 protein - yea
1135	63.5	5.3	1351	2	C71607	hypothetical prote
1136	63.5	5.3	1388	2	T17269	hypothetical prote
1137	63.5	5.3	1407	1	T00558	probable ABC trans
1138	63.5	5.3	1408	2	T47671	hypothetical prote
1139	63.5	5.3	1545	2	T47251	P-glycoprotein-lik
1140	63.5	5.3	1545	2	T42751	hypothetical prote
1141	63.5	5.3	1769	2	T46645	sulfonylurea recep
1142	63.5	5.3	2357	2	S53378	sulfonylurea recep
1143	63.5	5.3	4725	2	A59249	class VII unconven
1144	63	5.3	96	1	A44357	dynein heavy chain
1145	63.5	5.3	103	1	WMVZP3	F3 protein - fowlp
1146	63.5	5.3	175	2	T20878	hypothetical prote
1147	63.5	5.3	230	2	D70945	hypothetical prote
1148	63.5	5.3	230	2	B81705	conserved hypoth
1149	63.5	5.3	236	2	T17506	hypothetical prote
1150	63.5	5.3	249	2	F83520	phosphoribosylamin
1151	63.5	5.3	257	2	T01891	hypothetical prote
1152	63.5	5.3	258	2	S01165	achaete-scute locu
1153	63.5	5.3	258	2	H65188	sec-independent pr
1154	63.5	5.3	280	2	F86071	sec-independent pr
1155	63.5	5.3	280	2	H91224	Sec-independent pr
1156	63.5	5.3	288	2	S36954	maltose/maltodextr
1157	63.5	5.3	290	2	S48301	geranylgeranyl tra
1158	63.5	5.3	301	2	T50001	cytochrome-c oxida
1159	63.5	5.3	306	2	H83620	hypothetical prote
1160	63.5	5.3	313	2	A86743	probable permease
1161	63.5	5.3	322	2	B90013	hypothetical prote
1162	63.5	5.3	329	2	B87790	hypothetical prote
1163	63.5	5.3	332	2	B84943	conserved hypoth
1164	63.5	5.3	339	2	D89880	NADH2 dehydrogenas
1165	63.5	5.3	345	2	T12364	hypothetical prote
1166	63.5	5.3	358	2	B83808	probable serine/th
1167	63.5	5.3	359	2	S56720	prostaglandin E re
1168	63.5	5.3	361	2	A45211	surface adhesion h
1169	63.5	5.3	362	2	C69804	hypothetical prote
1170	63.5	5.3	362	2	T29552	hypothetical prote
1171	63.5	5.3	364	2	S65009	prostaglandin E re
1172	63.5	5.3	365	2	A42414	prostaglandin E re
1173	63.5	5.3	378	1	S17412	ubiquinol-cytochro
1174	63.5	5.3	379	1	S17411	ubiquinol-cytochro
1175	63.5	5.3	379	1	S41833	ubiquinol-cytochro
1176	63.5	5.3	379	2	S41847	ubiquinol-cytochro
1177	63.5	5.3	379	2	S43265	ubiquinol-cytochro
1178	63.5	5.3	379	2	T11492	ubiquinol-cytochro
1179	63.5	5.3	379	2	S58085	ubiquinol-cytochro
1180	63.5	5.3	379	2	S58464	ubiquinol-cytochro
1181	63.5	5.3	382	2	S47882	NADH2 dehydrogenas
1182	63.5	5.3	386	2	S47887	aromatic amino aci
1183	63.5	5.3	389	2	S60646	aspartate transami
1184	63.5	5.3	389	2	H95003	molybdopterin bios
1185	63.5	5.3	391	2	C97876	cell division prot
1186	63.5	5.3	396	2	E97947	proton/sodium-glut
1187	63.5	5.3	398	2	D64541	hypothetical prote
1188	63.5	5.3	405	2	B70415	arsenite transport
1189	63.5	5.3	411	2	T20902	corticotropin-rele
1190	63.5	5.3	415	2	G90154	cyclin Ia - maize
1191	63.5	5.3	420	2	A57742	hypothetical prote
1192	63.5	5.3	431	2	T23809	hypothetical prote
1193	63	5.3	448	2	T30982	hypothetical prote
1194	63	5.3	450	2	A34169	alpha-2A-adrenergi
1195	63	5.3	469	2	AE2188	hypothetical prote
1196	63	5.3	475	2	S52893	hypothetical prote
1197	63	5.3	478	2	C59095	hypothetical prote

No.			Len		Accession	Description
1198	63	5.3	480	2	B70367	hypothetical prote
1199	63	5.3	481	2	S60260	stomatin-like prot
1200	63	5.3	490	2	C71541	probable na-depend
1201	63	5.3	491	2	AC1499	transmembrane prot
1202	63	5.3	491	2	T02376	hypothetical prote
1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1204	63	5.3	508	2	E90594	transmembrane prot
1205	63	5.3	508	1	A48528	amino acid permeas
1206	63	5.3	527	2	T40744	membrane glycoprot
1207	63	5.3	531	2	AH1491	probable nuclear d
1208	63	5.3	531	2	T06153	hypothetical prote
1209	63	5.3	534	2	A99316	hypothetical prote
1210	63	5.3	535	2	AF1835	hypothetical prote
1211	63	5.3	562	2	T00081	hypothetical prote
1212	63	5.3	565	2	G84829	probable PTR2 fami
1213	63	5.3	569	2	G89789	probable PTR2 fami
1214	63	5.3	579	2	S66954	two-component sens
1215	63	5.3	583	2	B86359	two-component sens
1216	63	5.3	583	2	C70136	probable membrane
1217	63	5.3	584	2	B83875	protein Similar to
1218	63	5.3	598	2	T47566	flagellar basal-bo
1219	63	5.3	600	2	AD2000	two-component sens
1220	63	5.3	600	2	T26574	ABC transporter AT
1221	63	5.3	677	2	F95910	hypothetical prote
1222	63	5.3	677	2	H64485	probable membrane-
1223	63	5.3	682	1	T13568	replication licens
1224	63	5.3	701	2	T13665	NADH2 dehydrogenas
1225	63	5.3	702	2	T12677	NADH2 dehydrogenas
1226	63	5.3	704	2	T13665	NADH2 dehydrogenas
1227	63	5.3	712	2	D87418	NADH2 dehydrogenas
1228	63	5.3	729	2	T06127	proton pump, proba
1229	63	5.3	738	2	T06127	probable sugar tra
1230	63	5.3	738	2	S58612	S-protein secretio
1231	63	5.3	769	2	G95270	NADH2 dehydrogenas
1232	63	5.3	813	2	T02672	hypothetical prote
1233	63	5.3	849	2	C87740	protein H26021.2	
1234	63	5.3	869	2	S45082	probable membrane
1235	63	5.3	943	2	S49844	neurotrophic recep
1236	63	5.3	960	2	T17297	hypothetical prote
1237	63	5.3	1030	2	A42497	anion exchanger 3,
1238	63	5.3	1034	2	B86880	SWI/SNF family hel
1239	63	5.3	1082	2	H70360	cation efflux syst
1240	63	5.3	1082	2	B82809	exodeoxyribonuclea
1241	63	5.3	1212	2	B34911	DNA-damage-inducib
1242	63	5.3	1227	2	T18438	band 3-related pro
1243	63	5.3	1532	2	JH0422	hypothetical prote
1244	63	5.3	1646	2	T39035	hypothetical prote
1245	63	5.3	1854	2	T42742	voltage-dependent
1246	63	5.3	2203	2	B71621	putative sodium ch
1247	63	5.3	2295	2	RR1HM2	voltage-dependent
1248	63	5.3	4488	1	B69262	genome polyprotein
1249	63	5.2	107	2	B67739	hypothetical prote
1250	62.5	5.2	140	2	B38851	potassium channel
1251	62.5	5.2	149	2	JC1169	hypothetical prote
1252	62.5	5.2	168	2	D71702	hypothetical prote
1253	62.5	5.2	173	2	S67379	hypothetical prote
1254	62.5	5.2	178	2	G82911	hypothetical prote
1255	62.5	5.2	181	2	A11895	hypothetical prote
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1257	62.5	5.2	232	2	F83705	hypothetical prote
1258	62.5	5.2	236	2	H70091	hypothetical prote
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1260	62.5	5.2	245	2	S10658	hypothetical prote
1261	62.5	5.2	258	2	B91201	type III secretion
1262	62.5	5.2	274	2	A86048	ecr [imported] -
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1264	62.5	5.2	274	2	G72292	hypothetical prote
1265	62.5	5.2	276	2	G98336	hypothetical prote
1266	62.5	5.2	276	2	H83568	sorbitol/mannitol
1267	62.5	5.2	280	2	T11063	glycerol-3-phospha
1268	62.5	5.2	283	2	T14579	probable permease
1269	62.5	5.2	289	2	D82204	NADH2 dehydrogenas
1270	62.5	5.2	293	2	AH0075	phosphate ABC tran probable permease

ID	Score		Len	N	Accession	Description
1271	62.5	5.2	296	2	H83480	cytochrome o ubiqu
1272	62.5	5.2	298	2	T37251	homeobox protein c
1273	62.5	5.2	299	2	T26365	hypothetical prote
1274	62.5	5.2	326	2	C90272	hypothetical prote
1275	62.5	5.2	333	2	AB1925	ORF
1276	62.5	5.2	333	2	B89010	protein R08F11.2 [
1277	62.5	5.2	335	2	T41426	hypothetical wtf8
1278	62.5	5.2	349	2	H95060	ABC transporter, p
1279	62.5	5.2	349	2	D97929	hypothetical prote
1280	62.5	5.2	352	2	B81450	probable integral
1281	62.5	5.2	358	2	E81829	hypothetical prote
1282	62.5	5.2	365	2	F82210	amino acid ABC tra
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1284	62.5	5.2	370	2	C69309	conserved hypothet
1285	62.5	5.2	379	1	S17407	ubiquinol-cytochro
1286	62.5	5.2	379	2	S58462	ubiquinol-cytochro
1287	62.5	5.2	379	2	S58057	ubiquinol-cytochro
1288	62.5	5.2	382	2	A72373	conserved hypothet
1289	62.5	5.2	383	1	A44227	omega-3 fatty acid
1290	62.5	5.2	383	2	F84771	conserved hypothet
1291	62.5	5.2	383	2	T31738	hypothetical prote
1292	62.5	5.2	388	2	C64722	Na+/H+-exchanging
1293	62.5	5.2	391	2	A86632	aromatic amino aci
1294	62.5	5.2	399	2	H84087	sodium/glutamate s
1295	62.5	5.2	404	2	H83249	BBR3 protein - hu
1296	62.5	5.2	405	1	Q0BE35	protein T22F3.11	
1297	62.5	5.2	406	2	H89006	conserved hypothet
1298	62.5	5.2	409	2	C89942	conserved hypothet
1299	62.5	5.2	413	2	AC1369	multidrug resistan
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1301	62.5	5.2	420	2	D95018	conserved hypothet
1302	62.5	5.2	420	1	E97891	conserved hypothet
1303	62.5	5.2	422	2	C70518	hypothetical prote
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1305	62.5	5.2	426	2	F30010	flagellin limporte
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1307	62.5	5.2	431	2	E86542	CT266 hypothetical
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1311	62.5	5.2	443	2	E97172	probable omega-6 d
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1314	62.5	5.2	452	2	G85647	glycosyltransferas
1315	62.5	5.2	455	2	G90787	hypothetical prote
1316	62.5	5.2	457	2	D97217	UDP-N-acetylmuramo
1317	62.5	5.2	459	2	F69662	high-affinity bran
1318	62.5	5.2	461	2	AF3284	probable mannosyl
1319	62.5	5.2	468	2	S57713	inositol 1,4,5-tri
1320	62.5	5.2	470	2	A49131	hypothetical prote
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1322	62.5	5.2	490	2	S73161	hypothetical prote
1323	62.5	5.2	492	2	T40116	probable transmemb
1324	62.5	5.2	494	2	AC0768	hypothetical prote
1325	62.5	5.2	501	1	T15502	head protein gp5 -
1326	62.5	5.2	502	2	JN0539	hypothetical prote
1327	62.5	5.2	505	2	C86263	f42h10.1 protein -
1328	62.5	5.2	505	2	S44647	probable membrane
1329	62.5	5.2	507	2	S52677	probable membrane
1330	62.5	5.2	546	2	S64332	probable membrane
1331	62.5	5.2	547	2	S64567	hypothetical prote
1332	62.5	5.2	568	2	T22928	NADH2 dehydrogenas
1333	62.5	5.2	569	2	T11478	interleukin-10 rec
1334	62.5	5.2	572	2	I56215	hypothetical prote
1335	62.5	5.2	578	2	T02596	NADH2 dehydrogenas
1336	62.5	5.2	580	2	T11451	hypothetical prote
1337	62.5	5.2	601	2	T34391	NADH2 dehydrogenas
1338	62.5	5.2	608	2	A28798	myosin-light-chain
1339	62.5	5.2	610	2	B95897	hypothetical prote
1340	62.5	5.2	621	2	G02068	white homolog - hu
1341	62.5	5.2	638	2	C71868	probable cellulose
1342	62.5	5.2	668	2	T04073	intensifier 1 prot
1343	62.5	5.2	685	2	T19254	hypothetical prote
1344	62.5	5.2	704	2	S46000	probable membrane
1345	62.5	5.2	718	2	T05840	subtilisin-like pr
1346	62.5	5.2	763	2	T27937	hypothetical prote
1347	62.5	5.2	807	2	T28279	ORF MSV19 probabl
1348	62.5	5.2	815	2	G97266	mannose-1-phosphat
1349	62.5	5.2	837	2	D71027	hypothetical prote
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1351	62.5	5.2	865	2	AB1658	probable membrane
1352	62.5	5.2	881	2	G96574	hypothetical prote
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1355	62.5	5.2	1082	2	A81983	hypothetical prote
1356	62.5	5.2	1144	2	C87691	hypothetical prote
1357	62.5	5.2	1195	2	T17242	hypothetical prote
1358	62.5	5.2	1291	2	T20642	protein F09C3.1 [i
1359	62.5	5.2	1397	2	T21998	protein F09C3.1 [i
1360	62.5	5.2	1576	2	T21172	probable centromer
1361	62.5	5.2	1676	2	E71410	vitellogenin II pr
1362	62.5	5.2	1687	2	T43144	RNA viral polymera
1363	62.5	5.2	1951	2	B43963	hypothetical prote
1364	62.5	5.2	2150	2	S13553	NADH2 dehydrogenas
1365	62	5.2	112	2	T11073	cell-shape determi
1366	62	5.2	132	2	D82954	colicin B immunity
1367	62	5.2	174	2	B84028	uncharacterized co
1368	62	5.2	175	1	IMECB	hypothetical prote
1369	62	5.2	198	2	E97217	conserved hypothet
1370	62	5.2	201	2	G90134	protein F37C4.1 [i
1371	62	5.2	206	2	P89840	hypothetical prote
1372	62	5.2	209	2	A88656	type 4 prepilin-li
1373	62	5.2	209	2	B65127	probable phosphoes
1374	62	5.2	225	2	T32573	potassium channel
1375	62	5.2	242	1	F75433	dihydrolipoamide S
1376	62	5.2	247	2	AC1332	hypothetical prote
1377	62	5.2	273	2	E70010	probable sugar upt
1378	62	5.2	285	2	H95943	transcription regu
1379	62	5.2	287	2	A69838	cytochrome-c oxida
1380	62	5.2	288	2	S36938	probable permease
1381	62	5.2	298	2	C83356	hypothetical prote
1382	62	5.2	298	1	T29189	hypothetical prote
1383	62	5.2	305	2	T43972	conserved hypothet
1384	62	5.2	306	2	AI0209	chalcone reductase
1385	62	5.2	306	2	T41290	chalcone reductase
1386	62	5.2	312	2	S48849	conserved hypothet
1387	62	5.2	312	2	S48851	hypothetical prote
1388	62	5.2	315	2	T24821	hypothetical prote
1389	62	5.2	331	2	B57641	hypothetical prote
1390	62	5.2	344	2	T05987	F3H9.12 protein -
1391	62	5.2	345	2	T32203	hypothetical prote
1392	62	5.2	351	2	C86408	hypothetical prote
1393	62	5.2	352	2	C98170	interleukin-8 rece
1394	62	5.2	353	2	T42971	interleukin-8 rece
1395	62	5.2	360	2	S43611	hypothetical prote
1396	62	5.2	362	2	T33260	hypothetical prote
1397	62	5.2	370	2	S42379	G protein-coupled
1398	62	5.2	377	2	H84111	response regulator
1399	62	5.2	379	2	T05427	hypothetical prote
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1401	62	5.2	379	2	S58851	ubiquinol-cytochro
1402	62	5.2	381	2	E58851	ubiquinol-cytochro
1403	62	5.2	383	2	T11440	probable two-compo
1404	62	5.2	398	1	C95965	bicyclomycin resis
1405	62	5.2	399	2	E64112	hypothetical prote
1406	62	5.2	400	2	T72417	translocation prot
1407	62	5.2	402	2	JC5279	cell-division prot
1408	62	5.2	402	2	AB1565	xylose operon regu
1409	62	5.2	411	2	D70186	conserved hypothet
1410	62	5.2	411	2	B69338	cbs domain protein
1411	62	5.2	432	2	H72084	protein-tyrosine-p
1412	62	5.2	432	1	A34845	hypothetical prote
1413	62	5.2	435	2	T21880	hypothetical prote
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1415	62	5.2	444	2	F81367	hypothetical prote
1416	62	5.2	454	2	H65054	hypothetical prote

1417	62	5.2	458	2	A84487	probable replicati
1418	62	5.2	466	2	AH1800	transmembrane eff
1419	62	5.2	474	2	E64232	hypothetical prote
1420	62	5.2	483	2	S46124	nuclear protein EN
1421	62	5.2	487	1	T05271	probable 3-oxoacyl
1422	62	5.2	497	1	S53834	NADH2 dehydrogena
1423	62	5.2	497	2	S66834	probable membrane
1424	62	5.2	499	2	B81914	probable periplasm
1425	62	5.2	502	2	AE2372	hypothetical prote
1426	62	5.2	514	2	A96671	Ammonium transport
1427	62	5.2	528	1	ACCH2N	nicotinic acetylch
1428	62	5.2	555	2	T08869	protein P2 - Acyrt
1429	62	5.2	567	2	S29498	lymphocyte antigen
1430	62	5.2	582	2	S19424	hypothetical prote
1431	62	5.2	585	2	T02360	hypothetical prote
1432	62	5.2	600	2	H98149	ATP-binding transp
1433	62	5.2	600	2	AD3138	hypothetical prote
1434	62	5.2	630	2	H83686	PTS system, beta-g
1435	62	5.2	644	2	T20034	hypothetical prote
1436	62	5.2	660	2	A44432	amino acid transpo
1437	62	5.2	667	1	T20799	phosphotransferase
1438	62	5.2	675	2	S46952	hypothetical prote
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1440	62	5.2	678	2	T03903	hypothetical prote
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1442	62	5.2	707	2	A35804	heat shock protein
1443	62	5.2	724	1	HHMS84	hypothetical prote
1444	62	5.2	739	2	T25030	101K malaria antig
1445	62	5.2	743	2	A29232	probable ABC trans
1446	62	5.2	750	2	S73829	protein H06H21.10
1447	62	5.2	756	2	A88679	cytochrome-c oxida
1448	62	5.2	791	2	A46616	interleukin-4 rece
1449	62	5.2	810	2	A33380	vacuolar assembly
1450	62	5.2	841	2	T09455	aminopeptidase N |
1451	62	5.2	848	2	E95092	tegument protein 1
1452	62	5.2	864	2	T42556	97K alpha trans-in
1453	62	5.2	872	2	TNBEEH	otnA protein - Vib
1454	62	5.2	911	2	S70958	penicillin-binding
1455	62	5.2	932	2	C70191	Ca2+-transporting
1456	62	5.2	950	2	PWBYR1	conserved membrane
1457	62	5.2	1002	2	G97217	acriflavin resista
1458	62	5.2	1024	2	AE3557	Rab6 GTPase activa
1459	62	5.2	1030	2	T13163	hypothetical prote
1460	62	5.2	1031	2	T43458	hypothetical prote
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1462	62	5.2	1242	2	G88480	unknown protein F2
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1465	62	5.2	1321	2	A60165	hypothetical prote
1466	62	5.2	1780	2	T20695	hypothetical prote
1467	62	5.2	1802	2	T33783	bacitracin synthet
1468	62		6359	2	T31679	hypothetical prote
1469	61.5		99	2	B99233	hypothetical prote
1470	61.5		134	2	E69985	probable NADH2 deh
1471	61.5		149	2	C86655	hypothetical prote
1472	61.5		150	2	S43955	hypothetical prote
1473	61.5		159	2	S77185	lipoprotein signal
1474	61.5		162	2	AF2618	epithelial membran
1475	61.5		162	2	AF7400	hypothetical prote
1476	61.5		163	2	JC5045	hypothetical prote
1477	61.5		173	2	H97775	hypothetical prote
1478	61.5		176	2	G89947	hypothetical prote
1479	61.5		176	2	S40726	conserved hypothet
1480	61.5		183	2	H70478	hypothetical prote
1481	61.5		185	2	H69327	conserved hypothet
1482	61.5		190	2	A26630	nucleoplasmin A -
1483	61.5		212	2	A83521	conserved hypothet
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1486	61.5		272	2	G82888	hypothetical prote
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1488	61.5		274	2	S42168	NADH2 dehydrogenas
1489	61.5		276	2	F72342	conserved hypothet
1490	61.5	5.1	278	2	D83080	hypothetical prote
1491	61.5	5.1	279	2	AG0421	sugar transport sy
1492	61.5	5.1	284	2	AC3429	perosamine synthet
1493	61.5	5.1	289	2	F91269	hypothetical prote
1494	61.5	5.1	289	2	D86910	hypothetical prote
1495	61.5	5.1	290	2	D86910	ribonuclease BN (B
1496	61.5	5.1	290	2	AE0947	ribonuclease BN (B
1497	61.5	5.1	292	2	AE1539	sugar ABC transpor
1498	61.5	5.1	292	2	C90032	hypothetical prote
1499	61.5	5.1	293	2	A83710	ABC transporter (p
1500	61.5	5.1	293	2	B69866	transcription regu
	61.5	5.1	294	2	AD0886	probable oxidoredu

ALIGNMENTS

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Query Match           55.6%;   Score 664;   DB 2;   Length 445;
Best Local Similarity 56.2%;
Matches 135;  Conservative  38;  Mismatches  45;  Indels  22;  Gaps  5;
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RESULT 1
I38027
MLN 64 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: I38027; S60682
R;Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.
A;Title: Identification of four novel human genes amplified and overexpressed in breast c
Genomics 28, 367-376, 1995
A;Reference number: I37080; MUID:96039245; PMID:7490069
A;Accession: I38027
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-445 <RES>
A;Cross-references: UNIPARC:UPI000012F1BC; EMBL:X80198; NID:g951278; PIDN
A;Note: submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Gene: MLN64

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Qy  52 RRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFPLLAVFRFKVL 111
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Db  50 RRTFCLFVTFDLLFISLLWIIELNTNTGIRKNLEQEIIQVNFKTSFFDIFVLAFFRFSGL 109

Qy 112 ILAYAVCRLRHWWAIALTTAVTSAFLLAKYLILSKLFSQGAFGYVLDPIISFILAWIETWFL 171
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Db 110 LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAGYLLPIVSFVLAWLETWFL 169

Qy 172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGCQFYSPPESEAGSE-EAEEKQDSEK 229
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Db 170 DFKVLPQEAEEERWYLAAQVAVARGPLLF9GALSEGCQFYSPPESFAGSDNESDEEVAGKK 229
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RESULT 2
T16170
hypothetical protein F26F4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16170
R;Fulton, L.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F26F4.
A;Reference number: Z18471
A;Accession: T16170
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-478 <FUL>
A;Cross-references: UNIPROT:Q19819; UNIPARC:UPI000017B938; EMBL:U12964; NID:g1213452; PI...
C;Genetics:

A;Gene: CESP:F26F4.4
A;Introns: 47/3; 81/2; 125/3; 171/3; 214/2; 236/2; 343/3; 444/1

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Query Match             Score 204;  DB 2;  Length 478;
Best Local Similarity   17.1%;   26.5%;  Pred. No. 2.5e-11;
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Qy   42  GREKKGISDVRRTFCLFVTFDLLFVTLLWII----------------------ELNVNGGIENTLEK 86
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Db   69  GSQRIGVSKDRKRPIVITFFDTSITILILWLLCTVTRDDDWDKVFENEINI------------FNP 121

Qy   87  EVMQYDYSSYFDIFPLLAVFRKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKL 146
           :|| :                                            |::
Db  122  KFIRI--SLFDIVLLAVLRMLLIGVVVGICLVKQWYTVAFTLLASSAVILMKVLFYFN 177

Qy  147  FSQGAFGYVLPII-SFILAWIETWFLDFKVLPQEAEEENRLLIVQDDASERAALIPGGLSD 205
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Db  178  HSSSAVPPLLLIIITSFTLCWSEFYLMPFQILPRERYARREL------------DGIEN 224

Qy  206  GQFYSPPESEA---------------------GSEEAEEKQDSEKP 230
Db  225  PEFSTDDEARSNNRHRRGRRQQNSGNQSEAP 255
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RESULT 3
H9028I
hypothetical protein dppB-1 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H9028I
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H9028I
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <KUR>
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.J.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Cross-references: UNIPROT:Q97YQ0; UNIPARC:UPI00000643D5; GB:AE006641; NID:g13814471; E
A;Genetics:
A;Gene: dppB-1

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Query Match             Score 102.5;  DB 2;  Length 348;
Best Local Similarity   23.7%;   35%;  Pred. No. 0.064;
Matches   49;  Conservative   35;  Mismatches   66;  Indels   57;  Gaps   9;

Qy   15  SQSSHASLRNIHSINPTQLMARISYEGREKKGISDVRRTFCLFVTFDLLFVTLLWIIEL 74
Db   46  AQFSQTLFKNAHNLNSTOIQIAVEKY--RE------------------SLIAAYGL 81

Qy   75  NVNGGIENTLEK------EVMQYDYSSYFDIFPLLAVFRKVLILAYAVCRLRHWWAIAL 128
Db   82  N-----QPIIDKYFIQMYNLMRFDFGTAYF-LQAPSGSREVSSIIAYYLEN----TILL 130

Qy  129  TTAVTSAFLLAKVILSKLFSQGAF-GYVLPIISFILAWIETWFLDFKVLPQEAEEENRLL 187
Db  131  FFTTATIVFIVAGTIIGLLSAKSKFWEKVIAIIAVHSSIPTWWLGF------------VL 178

Qy  188  IVQDASERAALIPGGLSDGQFYSPPES 214
Db  179  IAALAYAVKVFPPGGMTS---VPPPKN 202
```

RESULT 4
D75080
glucose-1-phosphate thymidylyltransferase related protein PAB2433 - Pyrococcus abyssi (s
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D75080
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: D75080
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-424 <KAW>
A;Cross-references: UNIPROT:Q9UZW1; UNIPARC:UPI000003471C; GB:AJ248286; GB:AL096836; NID
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB2433
C;Superfamily: Aquifex aeolicus glucose-1-phosphate thymidylyltransferase

```
Query Match             Score 93.5;  DB 2;  Length 424;
Best Local Similarity   21.9%;   25%;  Pred. No. 0.57;
Matches   47;  Conservative   25;  Mismatches   72;  Indels   71;  Gaps   7;

Qy    5  PEDMENA----------------------LTGSQSSHASLRNIHSINPTQLMARIESYEGRE 44
Db  207  PEDIKKARKLIVYTSVKGVGDGPISRHLNRKISTRISALLVEHVTPNQM------------- 255

Qy   45  KKGISDVRRTFCLFVTFDL-LFVTLLWIIELNVNG---------------GIENTLEKEVMQYDY 93
Db  256  --------TIVTLFGIFSALMNFISVPIAGILYQVSSTLDGVDGEIARARMQTSK 303

Qy   94  YSSYFDIFPLLAVFRFK-VLILAYAVCRLRHWWAIALTTAVTSAFL---------------L 138
Db  304  FGGYFDSILDRYVDFTFLLILAVSIRRPLWWAIAAIAMFSSAMVSYSTERFKGAYCVDA 363

Qy  139  AKVI--LSKLFSQGAFGYVLPIISFILAWIETWFL 171
Db  364  YKVIPALRKVPGKDRERIFLTMLLTLVGWIKALFL 398
```

RESULT 5
T43048
calcium channel alpha-1 chain - Cyanea capillata
C;Species: Cyanea capillata
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43048
R;Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.
J. Biol. Chem. 273, 22792-22799, 1998
A;Title: Cloning and functional expression of a voltage-gated calcium channel alpha1 sub-
A;Reference number: Z22300; MUID:98380510; PMID:9712913
A;Accession: T43048
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1911 <JEZ>
A;Cross-references: UNIPROT:O02038; UNIPARC:UPI000007C488; EMBL:U93075; NID:g1947095; PII
A;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

```
Query Match             Score 90;  DB 2;  Length 1911;
Best Local Similarity   23.5%;   33%;  Pred. No. 7.2;
Matches   43;  Conservative   33;  Mismatches   59;  Indels   48;  Gaps   9;

Qy    5  PEDMENALTGSQSSHASLRNIHSINPTQLM----ARIESYEGREKKGISDV---------- 51
Db  791  PEDVE--LGNPKSKNGTLRHMGETTSTEMSEGRKEARIRPLRLSELNLLKDIDPMPPESS 848

Qy   52  --------RRTFCLFVTFDLLFVT--LLWIIELNVNGGIENTLEKEVMQYDYSSYFDI 100
Db  849  FFIFSANNKLRYLCYRLAVNKIFINSLVLIIMSSVALAAEDIGRDVLR-NKILGYFDI 907

Qy  101  FLLAVFRFKVLI--LAYAV-------CR----------LRHWWAIALTT-AVTSAFLLA 139
Db  908  FFTAMFTFEVTVKMIAFGVILHKRSFCRSFFNQLDLVIVAVSWAAIMLSRGSATSVVRIL 967

Qy  140  KVI 142
Db  968  RVL 970
```

RESULT 6

```
T21969
hypothetical protein F38E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Reference number: Z19495
C;Accession: T21969
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Status: preliminary; translated from GB/EMBL/DDBJ
R;Matthews, P.
submitted to the EMBL Data Library, January 1996
A;Molecule type: DNA
A;Residues: 1-767 <WIL>
A;Cross-references: UNIPROT:Q20170; UNIPARC:UPI000074B2B; EMBL:Z68342; PIDN:CAA92775.1;
.; Mole, S.E.
C;Genetics:
A;Experimental source: clone F38E11
A;Gene: CESP:F38E11.7
A;Map position: 4
A;Introns: 50/2; 118/1; 139/2; 169/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1; 6

Query Match          24.8%;  Score 86.5;  DB 2;  Length 767;
Best Local Similarity 24.8%;
Matches  35;  Conservative  22;  Mismatches  49;  Indels  35;  Gaps  5;

Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLIL---AYAV 117
Db  109 FDILLRSMLSFYE----DGVLITSFSETWRHYVHSFYFAIDLLAIFPFDYLLIRKTSAAF 164

Qy  118 CRLRHWW------------------------AIALTTAVTSAFLLAKVILSKLFSQGAFGVLPI 158

Qy  159 ISFILAW---IETWFLDFKVLP 177
Db  165 CRLNRFLKIYRIANFIAQSYGKLIQVTISLSKIFTACFLLFHV------NACVFYIISV 217

Db  218 NSDTSSWDGVNATFDDDEYLP 238


RESULT 7
B81299
probable molybdopterin biosynthesis protein Cj1519 [imported] - Campylobacter jejuni (st
C;Species: Campylobacter jejuni
A;Accession: B81299
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <PAR>
A;Cross-references: UNIPROT:Q9PME5; UNIPARC:UPI00000C1F59; GB:AL139078; GB:AL111168; NID
A;Experimental source: serotype O2; strain NCTC 11168
C;Genetics:
A;Gene: Cj1519
C;Superfamily: molybdenum cofactor molybdenum incorporation protein MoeA
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C;W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204

Query Match          21.0%;  Score 85.5;  DB 2;  Length 396;
Best Local Similarity 21.0%;
Matches  47;  Conservative  35;  Mismatches  81;  Indels  61;  Gaps  9;

Qy    4 LPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLF----- 58
Db  185 LGEALENPAQIRSSNHIAIANL----AKNLCNDTRVFPLLKDDEK 225

Qy   59 VTFDLLFVTLLWIIELNVNGGIE----NTLEKEVMQYDYSSYFDI------- 100
Db  226 ATFSTLESALQSCDILVTTGVSMGDFDFLKKAIKEYEIIIDKADIKPGRHIKIAKANEK 285

Qy  101 FLLAV--FRFKVLILAYAVCR--LRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVL 156
Db  286 FIIALPGFPYSAMVMFNLYTREILNSW-------LLQPKDVICKAFLQGSYKKKT 333
```

```
Qy  157 PIISFILAWIETWFLDFKVLPQ-EAEEENRLLIVQDASERAALI 199
Db  334 PYLEFVACNIE--FKNGRILANLEGKKEGSSAIINNLNNKAALM 375


RESULT 8
A57219
Batten disease-related protein CLN3 - human
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C;Accession: A57219
R;Lerner, T.J.; Boustany, R.M.N.; Anderson, J.W.; D'Arigo, K.L.; Schlumpf, K.; Buckler, 
E.M.; de Vos, N.; van Ommen, G.J.B.; Breuning, M.H.; Doggett, N.A.; Meincke, L.J.; Liu, 
.; Mole, S.E.
Cell 82, 949-957, 1995
A;Title: Isolation of a novel gene underlying Batten disease, CLN3.
A;Reference number: A57219
A;Accession: A57219
A;Cross-references: UNIPROT:Q13286; UNIPARC:UPI00000000ED; GB:U32680; NID:g1039422; PIDN
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-438 <LER>
A;Map position: 16p12.1-16p11.2
A;Cross-references: GDB:120593; OMIM:204200
A;Gene: GDB:CLN3
C;Genetics:
C;Superfamily: CLN3 protein/Battenin (Batten disease protein)
C;Keywords: membrane protein

Query Match          25.5%;  Score 85.5;  DB 2;  Length 438;
Best Local Similarity 25.5%;
Matches  38;  Conservative  18;  Mismatches  46;  Indels  47;  Gaps  8;

Qy   64 LFVTLLWII------------ELNVNGGI-----ENTLEKEVMQYDYSSYFDIFLLAVFRF 108
Db  277 VFKGLLWYIVPLVVVYFAEYPINQGLFELLFFWNTSLSHAQQYRWYQM---LYQAGVFAS 333

Qy  109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVLPIISFIL---- 163
Db  334 R--SSLRCCRIRFTWALALLQCLNLVFLLADV-------WFGF-LPSIYLVFLIILY 380

Qy  164 ------AWIETWFLDFKVLPQEAEEENR 185
Db  381 EGLLGGAAYVNT----FHNIALETSDEHR 405


RESULT 9
G70172
conserved hypothetical integral membrane protein BB0584 - Lyme disease spirochete
conserved hypothetical integral membrane protein (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Accession: G70172
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
A;Molecule type: DNA
A;Residues: 1-448 <KLE>
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Cross-references: UNIPROT:O51531; UNIPARC:UPI000005752F; GB:AE001160; GB:AE000783; NID
A;Experimental source: strain B31
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685

Query Match          24.4%;  Score 85;  DB 2;  Length 448;
Best Local Similarity 24.4%;
Matches  47;  Conservative  28;  Mismatches  64;  Indels  54;  Gaps  11;

Qy   50 DVRRTFCLFVTFDLLFVTL----LWIIELNVNGGIIE-NTLEKEVMQYDYSS------Y 97
Db  271 DTHKYAAYSISFIYFIFINIIHSFCISLNIMGYEMHNSKKEIMKVAIYLSKIGLKLAF 330
```

RESULT 10
A41680
integral membrane protein pssA - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 06-Oct-2000
R;Kuge, O.; Nishijima, M.; Akamatsu, Y.
J. Biol. Chem. 266, 24184-24189, 1991
A;Title: A Chinese hamster cDNA encoding a protein essential for phosphatidylserine synt
A;Reference number: A41680; MUID:92084729; PMID:1748687
A;Accession: A41680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-471 <KUG>
A;Cross-references: UNIPARC:UPI0000132B0F; GB:D10234; GB:D90468; NID:g220280; PIDN:BAA01
A;Superfamily: membrane protein
C;Keywords: membrane protein

Query Match   7.1%; Score 84.5; DB 2; Length 471;
Best Local Similarity   24.4%; Pred. No. 4.6;
Matches   32; Conservative   22; Mismatches   38; Indels   39; Gaps   7;

```
Qy    98 FDIFLLAVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVI--LSKLFSQGA---- 151
Db   331 LTSFVLFIFSFPAPVIFYTL-KYSHLIGIILRYSSVSAFFMALAFQYLFGFFRAGASPSF 389

Qy   152 FGYVLPIISFLLAWIETWFLDFKVLLPQEAEBEENRLLIV------QDASERAA 197
Db   390 GAIMEGSVTFVYIIP-IAFVLA------NYTNLPFE------IIVFIPSLEDAIKLVV 434

Qy   198 LIPGGLSDGQFYS 210
Db   435 SLP-----YFYS 441
```

RESULT 11
H97002
probable integral membrane protein [imported] - Clostridium acetobutylicum
A;Species: Clostridium acetobutylicum
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: UNIPROT:Q97KT1; UNIPARC:UPI00000C9FCF; GB:AE001437; PIDN:AAK78811.1;
A;Accession: H97002
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97002
A;Experimental source: Clostridium acetobutylicum ATCC824
A;Genetics:
A;Gene: CAC0835

Query Match   7.0%; Score 83.5; DB 2; Length 352;
Best Local Similarity   19.2%; Pred. No. 4.1;
Matches   38; Conservative   35; Mismatches   50; Indels   75; Gaps   8;

```
Qy    55 FCLFVTFDLLFVTLLMWIIELNVNGGIENTLEKEVMQY------------DYYSSYFDIFLLAV 105
Db   117 FLFLNFEQVKSLMYW-LDFNLRYA---TREADIMEYAVNCHVITWERIVSHFDIFAFGH 172

Qy   106 F----RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSLKFSQGAFGYVLPIISF 161
Db   173 FWGWAMKALLIRSYGLC-----WIISITWELTELF-------------FMHLLP-NF 210

Qy   162 ILAWIETWFLD 172
Db   211 AECWWDQVILD 221
```

RESULT 12
AE0302
sugar ABC transporter, permease protein YPO2476 [imported] - Yersinia pestis (strain CO92
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0302
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Cross-references: UNIPROT:Q82DT0; UNIPARC:UPI00000DCC19; GB:AL590842; PIDN:CAC91281.1;
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-291 <KUR>
A;Cross-references:
A;Genetics:
A;Gene: YP02476
C;Superfamily: inner membrane protein

Query Match   6.9%; Score 83; DB 2; Length 291;
Best Local Similarity   22.3%; Pred. No. 3.6;
Matches   44; Conservative   26; Mismatches   57; Indels   70; Gaps   10;

```
Qy    38 ESYEGREKKGISDVRRTFCLFVTFD--------------------------LLFYTLLWIEL 74
Db   115 EPYNVRDKKTNEDMKLLIKAVILVQNKTLNMERIVKDEQIGGLSKSERIIAFLIATVLLITS 174

Qy    75 NVNGGI-----------ENTLEKEVMQ-------------YDYYSSYFDIF----LLAVFRFKVL 111
Db   175 VVNGAVIIRDEBENTYYRYMXSPNSKPEYIFGNVIYNYIFSYIQLFIANSLMAIFGIYIG 234

Qy   112 I-----LAYAVCRLRHWWAIALTTAVTSAF-----LLAKVILSKLFSQGAFGYVLPIIS 160
Db   235 ISFLKMLSYGL---------ILTLVWTTFGTFIVCLFNKELYANMPSAA---------IS 276

Qy   161 FILAWIETWFLDFKVLPQ 178
Db   277 LILSLVGGTFINYKIMPE 294
```

RESULT 13
S34960
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion
C;Species: mitochondrion Crithidia oncopelti
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34960
R;Maslov, D.A.; Horvath, A.; Gwang II, K.; Kolesnikov, A.A.
submitted to the EMBL Data Library, October 1990
A;Reference number: S34960
A;Accession: S34960
A;Molecule type: DNA
A;Residues: 1-590 <MAS>
A;Cross-references: UNIPROT:Q34192; UNIPARC:UPI000008B400; EMBL:X56015; NID:g12879; PIDN
A;Genetics:

```
Qy    46 KGISDVRRTFCLFVTFDLLFVTLLWIIELNVN------GGIENTL 84
Db     9 KQVGSVLAASYLGYTSIFWFYFPFWLAVLSLTIEWRFVGIPTENGLNNFILVMQDPLFWKS 68

Qy    85 EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKV--- 141
Db    69 MLNVMRFLMY--YLPIVFISSFLF------AFGLQKLKHG-----RTFVALSFLLANVSSG 116

Qy   142 -----ILSKLFSQGA--------FGYVLPIIS-----FILAWIETW------FL 171
Db   117 VAYSIVFSKIFSQNGPLNTFLVDWFGFTLPWLTSPDFAMLSIALVVTWKFVGYYGLIFS 176

Qy   172 DFKVLPQE----AEEEN 184
Db   177 GLNSIPKEIYSAAELDN 193
```

A;Gene: ND5
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

```
Query Match       6.9%;  Score 83;  DB 1;  Length 590;
Best Local Similarity  23.9%;  Pred. No. 8.3;
Matches   32;  Conservative  23;  Mismatches  37;  Indels  42;  Gaps   7;

Qy    55 FCLFVTF-------DLL--FVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVF 106
            |:|              : |:|     :|:  :| ||:|   |||:
Db    95 FILFYAFYYMYYDLMLKRFENIFWWFVLCMWFFI--------LSYDYLFAYCGWELLGLF 146

Qy   107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFPGYVLPIISFILAWI 166
            :|:        |  :|  :| : ||| :|  : || |: :  ||||:|:||:|
Db   147 SF--PLISY----------------FWYRFFALKFGFKSFPISKI----------- 187

Qy   167 ET-------WFLDF 173
            :|        ||:|
Db   188 STGYGMINFYFVNF 201
```

RESULT 14
B29835
TraS protein - Escherichia coli plasmid pED208
C;Species: Escherichia coli
C;Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004
C;Accession: B29835
R;Finlay, B.B.; Paranchych, W.
J;Bacteriol. 166, 713-721, 1986
A;Title: Nucleotide sequence of the surface exclusion genes traS and traT from the IncF
A;Reference number: A29835; MUID:8623783; PMID:3011738
A;Accession: B29835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <FIN>
C;Cross-references: UNIPROT:P14498; UNIPARC:UPI000001563
C;Genetics:
A;Genome: plasmid

```
Query Match       6.9%;  Score 82.5;  DB 2;  Length 186;
Best Local Similarity  23.8%;  Pred. No. 2.4;
Matches   31;  Conservative  24;  Mismatches  40;  Indels  35;  Gaps   6;

Qy    61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLL----AVFRFKVLILAY 115
            |:||            |:|  :  ||   ::  |:            |  :|:|:|
Db    44 FQLLFI-----IFDIFINSNVR-------DYH--YFDTFVITLGSNAFFSLVFLMSTY 87

Qy   116 AVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFPGYVLPII----------SFILAW 165
            |||  : |  | :|| :||  :|| | : ||: :: |||
Db    88 NLVSLK----ISLGSEITEQSVLLKLVERKINSYGQFLMVVNAIVGCVLLSSGERFVAGL 143

Qy   166 IETWFLDFKV 175
            |:|::|:|
Db   144 GFSWFVTYLI 153
```

RESULT 15
C64227
hypothetical protein homolog MG247 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C64227
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M;Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: C64227
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-239 <TIGR>
C;Cross-references: UNIPROT:P47489; UNIPARC:UPI00001394F7; GB:U39703; GB:L43967; NID:g38
C;Genetics:
A;Experimental source: strain G-37
C;Genetic code: SGC3
C;Superfamily: Escherichia coli ygiH protein

```
Query Match       6.9%;  Score 82.5;  DB 1;  Length 239;
Best Local Similarity  21.7%;  Pred. No. 3.2;
Matches   33;  Conservative  26;  Mismatches  54;  Indels  39;  Gaps   8;

Qy    42 GREKKGISDVRRTF-----------CLFVTFDLLFVTLL--WIIELNVNGGIENTLEKEVMQYD 92
            | ||: :|: |           |||:|| |:||   |:|    |::  ||
Db    42 GSKNPGATNSMRVFGLKIGFLVAIFDPAFKGFFAFLITWIL---FFRGLQGYLTEKVYQST 98

Qy    93 YYSSYFDIFLLAV----------FRFK----VLILAYAVCRLRHWWAI----ALTTAVTSA 135
            |:||||:|||||          |:|      |:|||||||:|||:|:|      |:|||||
Db    99 YFLSYLSCFAATIGHIFPLYFKPKGGGKAIATTGGSLLAISLWWFLICLLIWIMITLITKY 158

Qy   136 FLLAKVILSKLFSQGAFPGYVLPIISFILAWIE 167
            |::|:: | |::  :||||||||||||::||:
Db   159 VSLASLITF-------FVLAVI-ILIPWLD 180
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Search completed: May 12, 2006, 20:44:15
Job time : 82 secs

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OM protein - protein search, using sw model

Run on:          May 12, 2006, 20:38:52 ; Search time 228 Seconds
                                            (without alignments)
                                            724.095 Million cell updates/sec

Title:           US-10-063-518-14
Perfect score:   1195
Sequence:        1 MNHLPEDMENALTGSQSSHA.........EAGSEEAEEKQDSEKPLLEL 234

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:   2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :       UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1195	100.0	234	1	MENTO_HUMAN	O95772 homo sapien
2	1141.5	95.5	235	2	Q5U205_RAT	Q5U205 rattus norv
3	1134.5	94.9	235	1	MENTO_MOUSE	Q9DC13 mus musculu
4	796	66.6	227	2	Q6DI38_BRARE	Q6DI38 brachydanio
5	700.5	58.5	448	2	Q6DFR7_XENTR	Q6DFR7 xenopus tro
6	698.5	58.5	448	2	Q6PF40_XENLA	Q6PF40 xenopus lae
7	684	57.2	444	2	Q6GNT3_XENLA	Q6GNT3 xenopus lae
8	684	55.6	445	1	MLN64_HUMAN	O14849 homo sapien
9	664	55.6	445	1	Q5XY53_HUMAN	Q5XY53 homo sapien
10	664	54.9	446	1	MLN64_MOUSE	Q61542 mus musculu
11	664	54.9	446	1	Q61542_MOUSE	Q61542 mus musculu
12	656.5	54.9	446	1	Q53Y53_HUMAN	Q53Y53 homo sapien
13	656.5	52.9	448	2	Q5U2T5_RAT	Q5U2T5 rattus norv
14	656.5	49.1	444	1	Q544C3_MOUSE	Q544C3 mus musculu
15	632	47.4	444	2	MLN64_BRARE	Q4S943 brachydanio
16	586.5	41.2	501	2	Q4S943_TETNG	Q4S943 tetraodon n
17	566	30.5	107	2	Q5RB70_PONPY	Q5RB70 pongo pygma
18	492	30.5	574	2	Q8BMP8_MOUSE	Q8BMP8 mus muscu
19	364.5	29.0	574	2	Q563D1_AEDAE	Q563D1 aedes aegyp
20	364.5	28.7	523	2	Q563D0_AEDAE	Q563D0 aedes aegyp
21	346	28.7	583	2	Q7QIT3_ANOGA	Q7QIT3 anopheles g
22	343	28.7	583	2	Q8MZH4_DROME	Q8MZH4 drosophila
23	343	22.8	131	2	Q9W145_DROME	Q9W145 drosophila
24	342.5	17.3	197	2	Q4THH5_TETNG	Q4THH5 tetraodon n
25	272	17.1	419	2	Q4SNJ2_TETNG	Q4SNJ2 tetraodon n
26	206.5	15.2	447	2	Q60Z70_CAEBR	Q60Z70 caenorhabdi
27	204	8.7	141	2	Q19819_CAEEL	Q19819 caenorhabdi
28	181.5	8.7	294	1	Q4SNJ3_TETNG	Q4SNJ3 tetraodon n
29	104.5	8.6	348	2	MLN64_SALPO	salvelinus
30	104.5	8.3	1095	2	Q97YQ0_SULSO	Q97YQ0 sulfolobus
31	102.5	8.1	714	2	Q4N7C1_THEPA	Q4N7C1 theileria p
32	99.5	7.8	714	2	Q5LPT4_SILPO	Q5LPT4 silicibacte
33	96.5 / 93.5	7.8	424	2	Q9UZW1_PYRAB	Q9UZW1 pyrococcus
32	93.5	7.8	438	1	CLN3_MACFA	Q60H10 macaca fasc
33	93.5	7.8	564	2	Q8HQ10_THRIM	Q8HQ10 thrips imag
34	90.5	7.8	246	2	Q8DU10_STRMU	Q8DU10 streptococc
35	90	7.6	525	2	Q7VFT4_HELIP	Q7VFT4 helicobacte
36	91	7.6	651	2	Q8DZX0_STRAS	Q8DZX0 streptococc
37	91	7.6	651	2	Q8E5M0_STRA3	Q8E5M0 streptococc
38	90.5	7.6	262	2	Q7NBJ4_MYCGA	Q7NBJ4 mycoplasma
39	90.5	7.6	530	1	O54F03_DICDI	O54F03 dictyosteli
40	90	7.5	1911	2	O02038_CYACP	O02038 cyanea capi
41	89.5	7.5	233	2	Q6JCT3_9HEMI	Q6JCT3 aleurodicus
42	89.5	7.5	367	2	Q6JCT6_9HEMI	Q6JCT6 aleurodicus
43	89.5	7.5	376	2	Q6HEH8_9ACAR	Q6HEH8 varroa dest
44	89.5	7.5	478	2	Q60IN0_CAEBR	Q60IN0 caenorhabdi
45	89.5	7.5	488	2	Q840W7_STRMU	Q840W7 streptococc
46	89	7.4	373	2	Q7RTB5_PLAYO	Q7RTB5 plasmodium
47	89	7.4	387	2	Q568R5_BRARE	Q568R5 brachydanio
48	89	7.4	387	2	Q5K830_CRYNE	Q5K830 cryptococcu
49	89	7.4	912	2	Q4YCI1_PLABE	Q4YCI1 plasmodium
50	88.5	7.4	384	2	Q6WNV4_RANCA	Q6WNV4 rana catesb
51	88	7.4	755	2	Q60QU6_CAEBR	Q60QU6 caenorhabdi
52	87.5	7.3	396	2	Q4HDY8_CAMCO	Q4HDY8 campylobact
53	87.5	7.3	473	2	Q640E5_CHICK	Q640E5 gallus gall
54	87	7.3	304	2	Q52M65_CHICK	Q52M65 gallus gall
55	87	7.3	610	2	Q640E5_XENLA	Q640E5 xenopus lae
56	87	7.3	720	2	Q7RRS2_PLAYO	Q7RRS2 plasmodium
57	87	7.3	707	2	Q6GN42_XENLA	Q6GN42 xenopus lae
58	87	7.3	756	2	Q8PYM2_METMA	Q8PYM2 methanosarc
59	86.5	7.3	328	2	Q55IJ0_CRYNE	Q55IJ0 cryptococcu
60	86.5	7.2	626	2	Q7NLL9_GLOVI	Q7NLL9 gloeobacter
61	86.5	7.2	647	2	Q7Z205_CAEEL	Q7Z205 caenorhabdi
62	86.5	7.2	891	2	Q4YS44_PLABE	Q4YS44 plasmodium
63	86	7.2	1050	2	Q8JLA2_9POXV	Q8JLA2 ectromelia
64	86	7.2	1056	2	Q871G6_NEUCR	Q871G6 neurospora
65	86	7.2	1453	2	Q7S7L6_NEUCR	Q7S7L6 neurospora
66	86	7.2	2515	2	Q4PAR7_USTMA	Q4PAR7 ustilago ma
67	85.5	7.2	174	2	Q4S220_TETNG	Q4S220 tetraodon n
68	85.5	7.2	336	2	Q95086_HUMAN	Q95086 homo sapien
69	85.5	7.2	339	2	Q4Y634_PLACH	Q4Y634 plasmodium
70	85.5	7.2	339	2	Q95089_HUMAN	Q95089 homo sapien
71	85.5	7.2	396	2	Q9PME5_CAMJE	Q9PME5 campylobact
72	85.5	7.2	438	1	CLN3_HUMAN	Q13286 homo sapien
73	85.5	7.2	438	2	Q54959_HUMAN	Q54959 homo sapien
74	85.5	7.2	473	1	PTSS1_HUMAN	P48651 homo sapien
75	85.5	7.2	747	2	Q93GL8_SALTY	Q93GL8 salmonella
76	85	7.2	348	2	Q9SF17_ARATH	Q9SF17 arabidopsis
77	85	7.1	377	2	Q6I2C1_BACAN	Q6I2C1 bacillus an
78	85	7.1	448	2	Q5I531_BORBU	Q5I531 borrelia bu
79	85	7.1	797	2	O82GJ8_STRAW	O82GJ8 streptomyce
80	84.5	7.1	412	2	Q4ITL6_AZOVI	Q4ITL6 azotobacter
81	84.5	7.1	430	1	O5ZTB7_LEGPH	O5ZTB7 legionella
82	84.5	7.1	471	1	PTSS1_CRIGR	O00576 cricetulus
83	84.5	7.1	473	2	Q91H2_MOUSE	Q91h2 mus musculu
84	84.5	7.1	487	2	Q6A0E5_MOUSE	Q6a0e5 mus musculu
85	84.5	7.1	892	2	Q9JF90_VACCT	Q9jf90 vaccinia vi
86	84	7.1	493	2	Q6SU88_MANSM	Q6su88 mannheimia
87	84	7.1	1118	2	Q5CUX5_CRYPV	Q5cux5 cryptospori
88	84	7.1	3848	2	Q5HSR1_CAMJR	Q5hsr1 campylobact
89	84	7.0	396	2	Q9HJK8_THEAC	Q9hjk8 thermoplasm
90	83.5	7.0	469	2	Q7TSH7_MOUSE	Q7tsh7 mus musculu
91	83.5	7.0	1700	2	Q75JN1_DICDI	Q75jn1 dictyosteli
92	83.5	7.0	275	2	Q4YS32_PLABE	Q4ys32 plasmodium
93	83.5	7.0	303	2	Q8XIT3_CLOPE	Q8xit3 clostridium
94	83.5	7.0	303	2	Q6FNB8_CANGA	Q6fnb8 candida gla
95	83.5	7.0	352	2	O1LB40_ARATH	O1lb40 arabidopsis
96	83.5	7.0	355	2	Q97KT1_CLOAB	Q97kt1 clostridium
97	83.5	7.0	380	2	Q6KI24_MYCMO	Q6ki24 mycoplasma
98	83.5	7.0	429	2	Q97C55_THEVO	Q97c55 thermoplasm
99	83.5	7.0	429	2	Q5ESF1_VIBF1	Q5esf1 vibrio fisc
100	83.5	7.0	590	2	Q9CTA9_MOUSE	Q9cta9 mus musculu
101	83.5	7.0	499	2	Q8PCX2_MOUSE	Q8pcx2 mus musculu
102	83.5	7.0	662	2	Q88P20_PSEPK	Q88p20 pseudomonas
103	83.5	7.0	834	2	Q9JHF5_MOUSE	Q9jhf5 mus musculu

No.	%		Length	N	Accession	Organism
105	83.5	7.0	834	2	Q9JL12_MOUSE	mus musculu
106	83.5	7.0	834	2	Q91W06_MOUSE	mus musculu
107	83.5	7.0	1034	2	Q72ZB9_TRYCR	trypanosoma
108	83.5	7.0	2483	2	Q5CH29_CRYHO	cryptospori
109	83	6.9	238	2	Q6YR96_ONYPE	onion yello
110	83	6.9	248	2	Q8GC56_EUBAC	eubacterium
111	83	6.9	291	2	Q8ZDT0_YERPE	yersinia pe
112	83	6.9	438	2	Q5XIH8_RAT	rattus norv
113	83	6.9	589	2	Q7TMW1_MOUSE	mus musculu
114	83	6.9	590	2	O34192_CRION	crithidia o
115	83	6.9	1056	2	Q8C2V1_MOUSE	mus musculu
116	83	6.9	1388	2	Q5DU28_MOUSE	mus musculu
117	83	6.9	2661	2	Q7RMS4_PLAYO	plasmodium
118	82.5	6.9	174	2	P97231_9ENTR	salmonella
119	82.5	6.9	186	1	TRAS2_ECOLI	escherichia
120	82.5	6.9	186	1	Q7BBW2_SALTI	salmonella
121	82.5	6.9	239	1	Y247_MYCGE	mycoplasma
122	82.5	6.9	341	2	Q56918_YEREN	yersinia en
123	82.5	6.9	367	2	Q8HCK3_9ACAR	varroa dest
124	82.5	6.9	389	2	Q5FL80_LACAC	lactobacill
125	82.5	6.9	406	2	O87249_9LACT	lactococcus
126	82.5	6.9	419	2	O19134_RABIT	oryctolagus
127	82.5	6.9	471	2	Q9QW77_CRIGR	cricetulus
128	82.5	6.9	510	2	Q95OM6_9FUNG	rhizophydiu
129	82.5	6.9	604	2	Q8RHJ3_FUSNN	fusobacteri
130	82.5	6.9	717	1	P09130_ECOLI	escherichia
131	82.5	6.9	781	1	Q4U8E8_THEAN	theileria a
132	82.5	6.9	891	2	O57223_9POXV	vaccinia vi
133	82.5	6.9	891	2	Q6J3A9_9POXV	vaccinia vi
134	82.5	6.9	891	2	O80DW2_COWPX	cowpox viru
135	82.5	6.9	892	2	Q6RZH3_9POXV	rabbitpox v
136	82.5	6.9	894	2	O8QMU0_COWPX	cowpox viru
137	82.5	6.9	1022	2	Q8BV00_LACPL	lactobacill
138	82.5	6.9	156	1	O81501_9HEPC	hepatitis c
139	82.5	6.9	161	1	Q69UD2_ORYSA	oryza sativ
140	82.5	6.9	228	1	Q5E5D8_VIBF1	vibrio fisc
141	82.5	6.9	301	2	O8RLZ3_HAEIN	haemophilus
142	82	6.9	303	2	O89L18_BRAJA	bradyrhizob
143	82	6.9	316	2	Q61RL6_CAEBR	caenorhabdi
144	82	6.9	382	2	O50H88_PORGI	porphyromon
145	82	6.9	384	2	O50HU1_PORGI	porphyromon
146	82	6.9	461	2	Q6AHB8_LEIXX	leifsonia x
147	82	6.9	472	2	O70J50_HAEIN	haemophilus
148	82	6.9	581	2	O4RQN5_TETNG	tetraodon n
149	82	6.9	587	2	Q6C0H8_YARLI	yarrowia li
150	82	6.9	589	1	RGP1_MOUSE	mus musculu
151	82	6.9	589	2	Q91YS2_MOUSE	mus musculu
152	82	6.9	589	2	O8C2E3_MOUSE	mus musculu
153	82	6.9	589	2	Q6NZB5_MOUSE	mus musculu
154	82	6.9	646	2	Q6ZPH4_MOUSE	mus musculu
155	82	6.9	647	2	O8PXU3_METMA	methanoarc
156	82	6.9	647	2	O4HJJ3_CAMLA	campylobact
157	82	6.9	819	2	O4JCD0_SULAC	sulfolobus
158	82	6.9	989	2	Q6CDE6_YARLI	yarrowia li
159	82	6.9	1031	2	O8I564_PLAF7	plasmodium
160	82	6.9	1466	2	P78576_EMENI	emericella
161	82	6.9	1466	2	Q5AS02_EMENI	aspergillus
162	82	6.9	190	2	Q9KIA9_ECOLI	escherichia
163	82	6.9	283	2	O51D23_ENTHI	entamoeba h
164	82	6.9	297	2	Q9B893_9TREM	schistosoma
165	82	6.9	311	2	Q8CD14_MOUSE	mus musculu
166	82	6.9	349	1	RNFD_PASMU	pasteurella
167	82	6.9	352	2	Q9H7E5_HUMAN	homo sapien
168	82	6.9	387	2	O72CJ7_DESVH	desulfovibr
169	82	6.9	391	2	Q4VBD2_MOUSE	mus musculu
170	82	6.9	414	2	Q6PAH4_MOUSE	mus musculu
171	82	6.9	438	2	O8C5B1_MOUSE	mus musculu
172	82	6.9	438	2	O35934_MOUSE	mus musculu
173	81.5	6.8	447	2	Q7VRC0_CANBF	candidatus
174	81.5	6.8	465	2	O8O3C9_BRARE	brachydanio
175	81.5	6.8	519	2	Q9NVS8_HUMAN	homo sapien
176	81.5	6.8	577	2	Q6PI26_HUMAN	homo sapien
177	81.5	6.8	577	2	Q7Z748_HUMAN	homo sapien
178	81.5	6.8	645	2	Q67UO9_ORYSA	oryza sativ
179	81.5	6.8	716	2	Q8DLB4_SYNEL	synechococc
180	81.5	6.8	735	2	Q6B3Y6_ECOLI	escherichia
181	81.5	6.8	892	2	Q775R6_CAMPS	camelpox vi
182	81.5	6.8	892	2	Q8V2P5_CAMPM	camelpox vi
183	81.5	6.8	1092	2	Q755K6_ASHGO	ashbya goss
184	81.5	6.8	1472	2	Q48GG6_TETNG	tetraodon n
185	81.5	6.8	1480	2	Q7R3B6_GIALA	giardia lam
186	81.5	6.8	1659	2	Q5KGP3_CRYNE	cryptococcu
187	81.5	6.8	1692	2	Q55S96_CRYNE	cryptococcu
188	81	6.8	174	2	Q92Q69_ARATH	arabidopsis
189	81	6.8	242	2	Q6D043_ERWCT	erwinia car
190	81	6.8	322	2	Q4MPN6_BACCE	bacillus ce
191	81	6.8	322	2	Q63ET7_BACCZ	bacillus ce
192	81	6.8	483	2	Q5AL74_CANAL	candida alb
193	81	6.8	486	2	Q5A405_CANAL	candida alb
194	81	6.8	492	2	Q5ALJ4_CANAL	candida alb
195	81	6.8	510	1	YOU1_CAEEL	caenorhabdi
196	81	6.8	536	1	YHB7_YEAST	saccharomyc
197	81	6.8	548	2	P38745_YEAST	saccharomyc
198	81	6.8	554	2	Q8XSV5_RALSO	ralstonia s
199	80.5	6.7	599	1	Q51NH6_MAGGR	magnaporthe
200	80.5	6.7	805	2	Q8QRL8_9HEPC	hepatitis c
201	80.5	6.7	1633	2	Q8GRI8_9HEPC	hepatitis c
202	80.5	6.8	3010	2	P97066_SALMO	salmonella
203	80.5	6.8	174	2	O8TNE9_METAC	methanoarc
204	80.5	6.7	242	2	O9SNE5_ARATH	arabidopsis
205	80.5	6.7	322	2	Q56WV6_ARATH	arabidopsis
206	80.5	6.7	353	2	Q86KR8_DICDI	dictyosteli
207	80.5	6.7	366	2	Q9U9O9_SCHPO	schizosacch
208	80.5	6.7	396	1	BTN1_SCHPO	schizosacch
209	80.5	6.7	417	1	TNAB_PROVU	proteus vul
210	80.5	6.7	423	2	Q4K188_STRPN	streptococc
211	80.5	6.7	423	2	P28785_STRPN	streptococc
212	80.5	6.7	463	2	Q8Y988_LISMO	listeria mo
213	80.5	6.7	463	2	Q8Y988_LISMO	listeria mo
214	80.5	6.7	463	2	O5EAZ3_XENLA	xenopus lae
215	80.5	6.7	463	2	O54256_DICDI	dictyosteli
216	80.5	6.7	485	1	Q9G861_9EUKA	malawimonas
217	80.5	6.7	485	2	Q9G861_9EUKA	malawimonas
218	80.5	6.7	536	2	O46378_CHLTR	chlamydia t
219	80.5	6.7	548	1	O7RC45_PLAYO	plasmodium
220	80.5	6.7	554	1	Q91ME6_9REOV	human rotav
221	80.5	6.7	599	1	Q91ME6_9REOV	human rotav
222	80.5	6.7	644	1	P53925_YEAST	saccharomyc
223	80.5	6.7	644	1	YNL5_YEAST	saccharomyc
224	80.5	6.7	716	2	Q6B2V3_YEAST	saccharomyc
225	80.5	6.7	732	2	Q5JBP7_ECOLI	escherichia
226	80.5	6.7	738	2	Q5JBP7_ECOLI	escherichia
227	80.5	6.7	103	2	O6SIZ5_ECOLI	escherichia
228	80.5	6.7	1687	2	P22708_ECOLI	escherichia
229	80.5	6.7	1780	1	TRAD2_ECOLI	escherichia
230	80.5	6.7	103	2	Q9RX39_DEIRA	deinococcus
231	80.5	6.7	156	2	O81513_9HEPC	hepatitis c
232	80.5	6.7	197	2	O81513_9HEPC	hepatitis c
233	80	6.7	238	2	Q95KH1_MACFA	macaca fasc
234	80	6.7	255	2	O95KH1_MACFA	macaca fasc
235	80	6.7	197	2	O5QTD8_HUMAN	homo sapien
236	80	6.7	156	2	Q7YWX2_CAEEL	caenorhabdi
237	80	6.7	891	2	O51XQ4_MONPV	vaccinia vi
238	80	6.7	891	1	P16715_VACCV	vaccinia vi
239	80	6.7	891	2	O51XQ4_MONPV	monkeypox v
240	80	6.7	891	2	Q762Q5_9POXV	monkeypox v
241	80	6.7	891	2	O8V4W5_MONPV	monkeypox v
242	80	6.7	891	2	O8V4W5_MONPV	monkeypox v
243	80	6.7	599	2	O7SC49_NEUCR	neurospora
244	80	6.7	290	2	Q9ZT82_ARATH	arabidopsis
245	80	6.7	290	2	Q99UM2_STAAM	staphylococ
246	80	6.7	290	1	Q9C840_ARATH	staphylococ
247	80	6.7	343	2	RTM1_YEAST	rhodopirell
248	80	6.7	347	2	O73JA5_TREDE	treponema d
249	80	6.7	355	2	O7N4F8_PHOLL	photorhabdu
250	80	6.7	360	2	Q9H1X3_HUMAN	homo sapien

#					Accession	Description
251	80	6.7	388	2	O58427_PYRHO	pyrococcus
252	80	6.7	488	2	Q65O58_ORYSA	oryza sativ
253	80	6.7	540	2	Q6FXI7_CANGA	candida gla
254	80	6.7	554	2	Q4PC93_USTMA	ustilago ma
255	80	6.7	650	2	Q699F8_ANOGA	anopheles g
256	80	6.7	661	2	Q75SY6_ASHGO	ashbya goss
257	80	6.7	680	2	Q7VH08_HELHP	helicobacte
258	80	6.7	700	2	O72O2I_LISMF	listeria mo
259	80	6.7	893	2	Q4I7I8_GIBZE	gibberella
260	80	6.7	3010	2	Q9QIY9_9HEPC	hepatitis c
261	79.5	6.7	266	2	Q5IPF9_9RODE	perognathus
262	79.5	6.7	266	2	Q5IPF8_9RODE	perognathus
263	79.5	6.7	269	2	Q72ZB0_LISMF	listeria mo
264	79.5	6.7	307	2	Q89NC2_BRAJA	bradyrhizob
265	79.5	6.7	367	2	Q8ESY3_OCEIH	oceanobacil
266	79.5	6.7	379	2	Q50BJ9_9RODE	perognathus
267	79.5	6.7	391	2	Q6TY96_9BILA	xiphinema a
268	79.5	6.7	438	2	CLN3_CANFA	canis famil
269	79.5	6.7	463	2	Q92EI3_LISIN	listeria in
270	79.5	6.7	488	2	Q6QU7O_ASPNG	aspergillus
271	79.5	6.7	491	2	VIE1_HCMVT	human cytom
272	79.5	6.7	546	1	FLVC2_RAT	rattus norv
273	79.5	6.7	549	2	Q4Z2F3_PLABE	plasmodium
274	79.5	6.7	598	2	O51954_BORHE	borrelia he
275	79.5	6.7	649	2	Q6BZ08_DEBHA	debaryomyce
276	79.5	6.7	674	2	Q86P19_DROME	drosophila
277	79.5	6.7	726	2	Q9EUJ3_SALET	salmonella
278	79.5	6.7	732	2	Q5J497_SALCH	salmonella
279	79.5	6.7	748	2	Q4WB47_ASPFU	aspergillus
280	79.5	6.7	784	2	Q9VYYO_DROME	drosophila
281	79.5	6.7	818	2	Q8KDB0_CHLTE	chlorobium
282	79.5	6.7	818	2	Q5HXC6_CAMJR	campylobact
283	79.5	6.7	1708	2	Q4LE27_HUMAN	homo sapien
284	79.5	6.7	3409	2	Q7SI27_NEUCR	neurospora
285	79	6.7	114	2	Q6VRR6_HELPY	helicobacte
286	79	6.7	251	2	Q6M0I2_METMP	methanococc
287	79	6.7	300	2	Q80ZH3_9MURI	arvicanthis
288	79	6.7	308	2	Q8RGM6_FUSNN	fusobacteri
289	79	6.7	312	2	Q6KH29_MYCMO	mycoplasma
290	79	6.7	323	2	Q7KSI9_DROME	drosophila
291	79	6.7	349	1	RNFD_BUCAP	buchnera ap
292	79	6.7	356	2	Q5X8I4_LEGPA	legionella
293	79	6.7	356	2	Q7MG43_VIBVY	vibrio vuln
294	79	6.7	375	2	Q4ZXH6_PSESY	pseudomonas
295	79	6.7	375	2	Q887L9_PSESM	pseudomonas
296	79	6.7	443	2	Q523L2_MAGGR	magnaporthe
297	79	6.7	484	2	Q6NIE0_CORDI	corynebacte
298	79	6.7	754	2	Q5IPY0_MAGGR	magnaporthe
299	79	6.7	770	2	Q5LA24_BACFN	bacteroides
300	79	6.7	770	2	Q64QD3_BACFR	bacteroides
301	79	6.7	828	2	Q4RGA8_TETNG	tetraodon n
302	79	6.7	1531	2	Q96L95_HUMAN	homo sapien
303	79	6.7	1679	2	Q86TB3_HUMAN	homo sapien
304	79	6.7	1780	2	Q61T87_CAEBR	caenorhabdi
305	79	6.7	2751	2	Q4Y3S8_PLACH	plasmodium
306	79	6.7	3010	2	Q9J3H8_9HEPC	hepatitis c
307	79	6.7	3010	2	Q9QIZ0_9HEPC	hepatitis c
308	78.5	6.6	239	1	Y350_MYCPN	mycoplasma
309	78.5	6.6	263	2	Q4Z3F6_PLABE	plasmodium
310	78.5	6.6	266	2	Q5IPE7_9RODE	perognathus
311	78.5	6.6	269	2	Q92DL5_LISIN	listeria in
312	78.5	6.6	292	2	Q5V6V4_HALMA	haloarcula
313	78.5	6.6	313	2	Q9L0B3_STRCO	streptomyce
314	78.5	6.6	353	2	Q4HJT2_CAMLA	campylobact
315	78.5	6.6	358	1	RNFD_HAEIN	haemophilus
316	78.5	6.6	358	2	Q4QJQ5_HAEI8	haemophilus
317	78.5	6.6	380	2	Q8A8F8_BACTN	bacteroides
318	78.5	6.6	382	2	Q5LE17_BACFN	bacteroides
319	78.5	6.6	382	2	Q64V54_BACFR	bacteroides
320	78.5	6.6	418	2	Q65LP8_BACLD	bacillus li
321	78.5	6.6	451	2	Q65UD5_MANSM	mannheimia
322	78.5	6.6	471	1	P18599	cricetulus
323	78.5	6.6	512	2	Q8G1D7_BRUSU	brucella su

#					Accession	Description		
324	78.5	6.6	538	2	Q4HFH8_CAMCO	campylobact	Q4hfh8	campylobact
325	78.5	6.6	557	2	Q5CXU4_CRYPV	cryptospori	Q5cxu4	cryptospori
326	78	6.6	666	1	KUP_STRA5	streptococc	KUP_STRA5	streptococc
327	78	6.6	678	2	Q8DZI1_STRA5	streptococc	Q8dzi1	streptococc
328	78	6.6	678	1	Q61710_MOUSE	mus musculu	Q61710	mus musculu
329	78	6.6	683	2	Q769F3_HUMAN	homo sapien	Q769f3	homo sapien
330	78	6.6	726	2	Q769F4_HUMAN	homo sapien	Q769f4	homo sapien
331	78	6.6	766	1	ABCB9_HUMAN	homo sapien	ABCB9_HUMAN	homo sapien
332	78	6.6	769	2	Q6P2Q0_HUMAN	homo sapien	Q6p2q0	homo sapien
333	78.5	6.6	796	2	Q5W9G7_HUMAN	homo sapien	Q5w9g7	homo sapien
334	78.5	6.6	867	2	Q4N908_THEPA	theileria p	Q4n908	theileria
335	78.5	6.6	1308	2	Q4XVA2_PLACH	plasmodium	Q4xva2	plasmodium
336	78.5	6.6	6473	2	Q8IKH9_PLAF7	plasmodium	Q8ikh9	plasmodium
337	78	6.6	188	2	Q8IYM2_BACAN	bacillus an	Q8iym2	bacillus an
338	78	6.6	219	2	Q8W2Y0_ORYSA	oryza sativ	Q8w2y0	oryza sativ
339	78	6.6	226	2	Q7T829_9CORO	avian infec	Q7t829	avian infec
340	78	6.6	240	2	Q9CPF6_PASMU	pasteurella	Q9cpf6	pasteurella
341	78	6.6	245	2	P94625_CLODI	clostridium	P94625	clostridium
342	78	6.6	252	2	Q6B8K2_GRATL	gracillaria	Q6b8k2	gracillaria
343	78	6.6	252	2	Q9KD13_BACHD	bacillus ha	Q9kd13	bacillus
344	78	6.6	321	2	Q96XC4_SULTO	sulfolobus	Q96xc4	sulfolobus
345	78	6.6	339	2	Q8D4K9_VIBVU	vibrio vuln	Q8d4k9	vibrio vuln
346	78	6.6	357	2	Q5BJW9_RAT	rattus norv	Q5bjw9	rattus norv
347	78	6.5	360	2	Q95IA3_TETTH	tetrahymena	Q95ia3	tetrahymena
348	78	6.5	382	2	Q97HC3_CLOAB	clostridium	Q97hc3	clostridium
349	78	6.5	414	2	Q8TN61_METAC	methanosarc	Q8tn61	methanosarc
350	78	6.5	428	2	Q8D5Y9_VIBVU	vibrio vuln	Q8d5y9	vibrio vuln
351	78	6.5	431	2	Q9JRS0_ACTAC	actinobacil	Q9jrs0	actinobacil
352	78	6.5	442	2	Q7MD08_VIBVY	vibrio vuln	Q7md08	vibrio vuln
353	78	6.5	471	1	Y872_HAEIN	haemophilus	Y872_HAEIN	haemophilus
354	78	6.5	486	2	Q6HMA8_BACHK	bacillus th	Q6hma8	bacillus th
355	78	6.5	486	2	Q6FSM9_CANGA	candida gla	Q6fsm9	candida gla
356	78	6.5	641	2	Q9LIC2_ARATH	arabidopsis	Q9lic2	arabidopsis
357	78	6.5	658	2	Q7QGO8_ANOGA	anopheles g	Q7qgo8	anopheles g
358	78	6.5	658	2	Q98M77_RHILO	rhizobium l	Q98m77	rhizobium
359	78	6.5	1297	2	Q9Y817_SCHPO	schizosacch	Q9y817	schizosacch
360	78	6.5	2136	1	YCF2_MARPO	marchantia	YCF2_MARPO	marchantia
361	78	6.5	7180	1	R1AB_CVMJH	m replicase	R1ab_CVMJH	m replicase
362	77.5	6.5	176	2	Q976T7_SULTO	sulfolobus	Q976t7	sulfolobus
363	77.5	6.5	190	2	Q4MQY0_BACCE	escherichia	Q4mqy0	escherichia
364	77.5	6.5	263	2	Q73DX2_BACC1	bacillus ce	Q73dx2	bacillus ce
365	77.5	6.5	263	2	O81I83_BACCR	bacillus ce	O81i83	bacillus ce
366	77.5	6.5	266	2	Q5IPF6_PERLO	perognathus	Q5ipf6	perognathus
367	77.5	6.5	269	2	Q8Y8T5_LISMO	listeria mo	Q8y8t5	listeria mo
368	77.5	6.5	270	2	Q8HIY4_PERLO	perognathus	Q8hiy4	perognathus
369	77.5	6.5	270	2	Q8HIY5_PERLO	perognathus	Q8hiy5	perognathus
370	77.5	6.5	270	2	Q8HIY2_PERLO	perognathus	Q8hiy2	perognathus
371	77.5	6.5	270	2	Q8HIY1_PERLO	perognathus	Q8hiy1	perognathus
372	77.5	6.5	270	2	Q8HIY3_PERLO	perognathus	Q8hiy3	perognathus
373	77.5	6.5	294	2	Q8ET30_OCEIH	oceanobacil	Q8et30	oceanobacil
374	77.5	6.5	299	2	Q8ZAL1_YERPE	yersinia pe	Q8zal1	yersinia pe
375	77.5	6.5	299	2	Q66FT9_YERPS	yersinia ps	Q66ft9	yersinia ps
376	77.5	6.5	299	2	Q8D1I6_YERPE	yersinia pe	Q8d1i6	yersinia pe
377	77.5	6.5	310	2	Q9PQG1_UREPA	ureaplasma	Q9pqg1	ureaplasma
378	77.5	6.5	328	2	Q9K686_BACHD	bacillus ha	Q9k686	bacillus ha
379	77.5	6.5	328	2	Q42882_SCHPO	schizosacch	Q42882	schizosacch
380	77.5	6.5	365	2	Q8R770_THETN	thermoanaer	Q8r770	thermoanaer
381	77.5	6.5	377	2	Q4R2P6_VARHI	vargula hil	Q4r2p6	vargula hil
382	77.5	6.5	377	2	Q4R2A7_VARHI	vargula hil	Q4r2a7	vargula hil
383	77.5	6.5	377	2	Q4R264_VARHI	vargula hil	Q4r264	vargula hil
384	77.5	6.5	377	2	Q4R1X9_VARHI	vargula hil	Q4r1x9	vargula hil
385	77.5	6.5	377	2	Q4R1V7_VARHI	vargula hil	Q4r1v7	vargula hil
386	77.5	6.5	377	2	Q4R2P5_VARHI	vargula hil	Q4r2p5	vargula hil
387	77.5	6.5	379	2	Q48008_PERLO	perognathus	Q48008	perognathus
388	77.5	6.5	392	2	Q6G7P7_BIFLO	bifidobacte	Q6g7p7	bifidobacte
389	77.5	6.5	411	2	Q9P6N5_SCHPO	schizosacch	Q9p6n5	schizosacch
390	77.5	6.5	416	2	Q4YTQ0_PLABE	plasmodium	Q4ytq0	plasmodium
391	77.5	6.5	422	2	Q9HKX6_THEAC	thermoplasm	Q9hkx6	thermoplasm
392	77.5	6.5	430	2	Q5WUJ7_LEGPL	legionella	Q5wuj7	legionella
393	77.5	6.5	440	2	Q9ZY23_PEDMN	pedinomonas	Q9zy23	pedinomonas
394	77.5	6.5	481	2	Q62XT1_BACLD	bacillus li	Q62xt1	bacillus li
395	77.5	6.5	481	2	Q4P6B0_USTMA	ustilago ma	Q4p6b0	ustilago ma
396	77.5	6.5	483	2	Q9G8V8_9CRYP	rhodomonas	Q9g8v8	rhodomonas

#					Accession	Description
397	77.5	6.5	491	2	O28284_ARCFU	archaeoglob
398	77.5	6.5	491	2	Q6SX10_HCMV	human cytom
399	77.5	6.5	512	2	Q57DX0_BRUAB	brucella ab
400	77.5	6.5	512	2	Q8YGI2_BRUME	brucella me
401	77.5	6.5	538	2	Q4HP2_CAMUP	campylobact
402	77.5	6.5	556	2	Q89180_VARV	variola vir
403	77.5	6.5	556	2	Q89232_VARV	variola vir
404	77.5	6.5	567	2	Q7RNK0_PLAYO	plasmodium
405	77.5	6.5	572	2	Q4X2G8_PLACH	plasmodium
406	77.5	6.5	618	2	Q59P22_CANAL	candida alb
407	77.5	6.5	620	2	Q8EKA1_SHEON	shewanella
408	77.5	6.5	676	1	Q4RUC5_TETNG	tetraodon n
409	77.5	6.5	734	1	NU5C_ORYSA	oryza sativ
410	77.5	6.5	788	1	Q4RUC9_TETNG	tetraodon n
411	77.5	6.5	892	1	P33817_VARV	variola vir
412	77.5	6.5	892	2	Q9QNI0_VARV	variola vir
413	77.5	6.5	979	2	Q7MLV5_VIBVY	vibrio vuln
414	77.5	6.5	1033	2	Q5BL65_XENTR	xenopus tro
415	77.5	6.5	1140	2	Q5CTR7_CRYPV	cryptospori
416	77.5	6.5	1476	2	Q8ST66_DICDI	dictyosteli
417	77.5	6.5	1784	2	Q2S377_LOLOP	loligo opal
418	77.5	6.5	1959	2	Q5ZSB8_ORYSA	oryza sativ
419	77.5	6.5	2141	2	Q86H92_LYMST	lymnaea sta
420	77.5	6.5	6680	2	Q5CXT7_CRYPV	cryptospori
421	77	6.4	170	2	Q72UC4_LEPIC	leptospira
422	77	6.4	170	2	Q7MXQ0_PORGI	porphyromon
423	77	6.4	255	2	Q98VN5_EAV	equine arte
424	77	6.4	286	2	Q61082_BACAN	bacillus an
425	77	6.4	286	2	Q73A28_BACC1	bacillus ce
426	77	6.4	287	2	Q54LT2_DICDI	dictyosteli
427	77	6.4	315	2	Q4HFE7_CAMCO	campylobact
428	77	6.4	332	2	Q9XTH3_CAEEL	caenorhabdi
429	77	6.4	353	1	MTR1A_MOUSE	mus musculu
430	77	6.4	379	2	Q8WEK6_THOTA	thomomys ta
431	77	6.4	383	2	Q8TZC2_METKA	methanopyru
432	77	6.4	386	2	P94949_METKA	methanopyru
433	77	6.4	419	2	Q7MXQ0_PORGI	porphyromon
434	77	6.4	423	2	Q71X88_LISMF	listeria mo
435	77	6.4	430	2	Q8U1Z6_PYRFU	pyrococcus
436	77	6.4	435	2	Q73RD9_TREDE	treponema d
437	77	6.4	444	2	Q6GD70_STAAS	staphylococ
438	77	6.4	444	2	Q8NYX5_STAAM	staphylococ
439	77	6.4	481	2	Q4WQW3_ASPFU	aspergillus
440	77	6.4	490	2	O14670_HUMAN	homo sapien
441	77	6.4	491	2	Q9T251_PHYIN	phytophthor
442	77	6.4	505	2	Q4U156_THEAN	theileria a
443	77	6.4	519	2	Q9ASQ7_ARATH	arabidopsis
444	77	6.4	537	2	Q518N5_ENTHI	entamoeba h
445	77	6.4	559	2	Q9AAX4_CAUCR	caulobacter
446	77	6.4	590	1	Q4NSD5_9DELT	anaeromyxob
447	77	6.4	606	2	Q5W2R7_SULIS	sulfolobus
448	77	6.4	616	2	Q5WG33_STAAS	staphylococ
449	77	6.4	650	2	Q6G633_STAAS	staphylococ
450	77	6.4	650	2	Q6GDG1_STAAR	staphylococ
451	77	6.4	650	2	Q5HCQ6_STAAC	staphylococ
452	77	6.4	650	2	Q7A374_STAAN	staphylococ
453	77	6.4	650	2	Q8NUK4_STAAW	staphylococ
454	77	6.4	722	2	Q99QZ7_STAAM	staphylococ
455	77	6.4	738	2	Q632R1_BACC2	bacillus ce
456	77	6.4	789	1	Q8L838_ARATH	arabidopsis
457	77	6.4	789	1	FTSK_STAAW	staphylococ
458	77	6.4	836	2	Q7Z1F2_PLAFA	plasmodium
459	77	6.4	877	2	Q7Z1F2_PLAFA	plasmodium
460	77	6.4	991	2	O81330_ARATH	arabidopsis
461	77	6.4	1024	2	Q7Z1F1_PLAFA	plasmodium
462	77	6.4	1024	2	Q7ZIF1_PLAFA	plasmodium
463	77	6.4	1025	2	Q1K26_PLAF7	plasmodium
464	77	6.4	1117	2	Q25693_PLAFA	plasmodium
465	77	6.4	1477	2	Q9M133_ARATH	arabidopsis
466	77	6.4	1500	2	Q6FTR9_CANGA	candida gla
467	77	6.4	1814	2	Q9ZU84_ARATH	arabidopsis
468	77	6.4	3010	2	Q60WH4_CAEBR	caenorhabdi
469	77	6.4	3010	2	Q68788_9HEPC	hepatitis c
470	77	6.4	3010	2	Q81757_9HEPC	hepatitis c
471	77	6.4	3010	2	Q9J3G4_9HEPC	hepatitis c
472	77	6.4	3013	2	Q6J6P5_9HEPC	hepatitis c
473	77	6.4	3013	2	Q9J3F3_9CORO	murine hepa
474	77	6.4	4416	2	Q9J3F8_9CORO	murine hepa
475	77	6.4	4416	2	Q9PYA3_	m replicase
476	76.5	6.4	7124	1	R1AB_CVM2	murine hepa
477	76.5	6.4	253	2	Q5IPE6_PERLO	perognathus
478	76.5	6.4	266	2	Q5IPE8_PERLO	perognathus
479	76.5	6.4	278	2	Q8XBF0_ECO57	escherichia
480	76.5	6.4	278	2	Q8XBF0_ECO57	escherichia
481	76.5	6.4	281	2	Q8KS89_9BILA	ancylostoma
482	76.5	6.4	282	2	Q92WV5_RHIME	rhizobium m
483	76.5	6.4	342	2	Q7Z290_CAEEL	caenorhabdi
484	76.5	6.4	352	1	RNFD_SALTI	salmonella
485	76.5	6.4	352	2	Q57PI1_SALCH	salmonella
486	76.5	6.4	352	2	Q8ZPM3_SALTY	salmonella
487	76.5	6.4	379	2	Q5PIC8_SALPA	salmonella
488	76.5	6.4	379	1	CYB_DIPOR	dipodomys o
489	76.5	6.4	379	2	Q9GBY7_OCHPA	ochotona pa
490	76.5	6.4	379	2	Q50818_9RODE	dipodomys m
491	76.5	6.4	379	2	Q50818_9RODE	dipodomys m
492	76.5	6.4	379	2	Q508J5_PERLO	perognathus
493	76.5	6.4	380	2	Q508J3_9RODE	perognathus
494	76.5	6.4	391	2	Q8HNI7_PRANA	pronays nat
495	76.5	6.4	391	2	Q4SIZ9_TETNG	tetraodon n
496	76.5	6.4	395	2	Q62GZ4_ORYSA	oryza sativ
497	76.5	6.4	415	2	Q82V00_NITEU	nitrosomona
498	76.5	6.4	415	1	Q19084_CAEBR	caenorhabdi
499	76.5	6.4	415	2	Q5UES7_ECOLI	escherichia
500	76.5	6.4	438	1	Q8KHK2_PSEAE	pseudomonas
501	76.5	6.4	439	2	Q7UB13_SHIFL	shigella fl
502	76.5	6.4	439	2	Q83PL5_SHIFL	shigella fl
503	76.5	6.4	451	2	Q83P15_SHIFL	shigella fl
504	76.5	6.4	462	1	Q61124_MOUSE	mus musculu
505	76.5	6.4	490	2	Q61124_MOUSE	mus musculu
506	76.5	6.4	491	2	Q5LBQ8_BACFN	bacteroides
507	76.5	6.4	500	1	Q64SN0_BACFR	bacteroides
508	76.5	6.4	526	2	Q64SN0_BACFR	bacteroides
509	76.5	6.4	526	2	Q660T8_BORGA	borrelia ga
510	76.5	6.4	528	2	Q660T8_BORGA	borrelia ga
511	76.5	6.4	538	2	Q9PIV5_CAMJE	campylobact
512	76.5	6.4	538	2	Q9PIV5_CAMJR	campylobact
513	76.5	6.4	560	2	Q8NBG4_HUMAN	homo sapien
514	76.5	6.4	570	2	Q7Z6J6_HUMAN	homo sapien
515	76.5	6.4	580	2	Q627P1_CAEBR	caenorhabdi
516	76.5	6.4	614	2	Q7Z6J6_HUMAN	homo sapien
517	76.5	6.4	614	2	Q9ZLN1_HELPJ	helicobacte
518	76.5	6.4	615	2	Q9ZLN1_HELPJ	helicobacte
519	76.5	6.4	649	2	Q577U9_BRUAB	brucella ab
520	76.5	6.4	687	2	Q8FWB2_BRUSU	brucella su
521	76.5	6.4	743	2	Q577U9_BRUAB	brucella ab
522	76.5	6.4	775	2	Q4N6A4_THEPA	theileria p
523	76.5	6.4	839	2	Q5ZTF9_CHICK	gallus gall
524	76.5	6.4	902	2	Q4IIV8_GIBZE	gibberella
525	76.5	6.4	909	2	Q54BU4_DICDI	dictyosteli
526	76.5	6.4	909	2	Q8T9W6_DICDI	dictyosteli
527	76.5	6.4	1485	2	Q8EUA2_MYCPE	mycoplasma
528	76.5	6.4	1641	2	Q6BS27_DEBHA	debaryomyce
529	76.5	6.4	156	2	Q81504_9HEPC	hepatitis c
530	76	6.4	201	2	Q6MT09_MYCMS	mycoplasma
531	76	6.4	210	2	Q8PXL0_METMA	methanosarc
532	76	6.4	255	2	Q6V7I5_EAV	equine arte
533	76	6.4	272	2	Q8R7J2_THETN	thermoanaer
534	76	6.4	292	2	Q8ELU4_OCEIH	oceanobacil
535	76	6.4	325	2	Q9ZZH9_MESAU	mesocricetu
536	76	6.4	346	1	NU2M_LOCMI	locusta mig
537	76	6.4	346	2	Q4H7X1_9DEIO	deinococcus
538	76	6.4	402	2	Q21933_CAEEL	caenorhabdi
539	76	6.4	425	2	Q9JRS2_ACTAC	actinobacil
540	76	6.4	438	2	Q88HG7_PSEPK	pseudomonas
541	76	6.4	461	2	Q85002_STRPN	streptococc
542	76	6.4	474	2	Q8F2K0_LEPIN	leptospira

No.			Len	n	ID	Organism
543	76	6.4	474	2	Q72SX4_LEPIC	q72sx4 leptospira
544	76	6.4	519	2	Q85P3_PERFR	q85p3 perilla fru
545	76	6.4	567	2	Q6NXT6_HUMAN	q6nxt6 homo sapien
546	76	6.4	616	2	Q7QWH6_GIALA	q7qwh6 giardia lam
547	76	6.4	699	2	Q9LZZ7_ARATH	q9lzz7 arabidopsis
548	76	6.4	699	2	Q6IVM6_9GAMM	q6ivm6 uncultured
549	76	6.4	851	2	Q6CKO4_KLULA	q6cko4 kluyveromyc
550	76	6.4	931	2	Q7NBN0_MYCGA	q7nbn0 mycoplasma
551	76	6.4	953	2	Q5Z570_ORYSA	q5z570 oryza sativ
552	76	6.4	1046	2	Q7PVU9_ANOGA	q7pvu9 anopheles g
553	76	6.4	1301	1	DHX9_CAEEL	dhx9 caenorhabdi
554	76	6.4	1450	1	CFTR_RABIT	cftr rabbit
555	76	6.4	1481	2	Q9TTX9_RABIT	q9ttx9 rabbit
556	76	6.4	1551	2	Q96WN4_VENIN	q96wn4 venturia in
557	76	6.4	1783	2	O18698_CAEEL	o18698 caenorhabdi
558	76	6.4	1877	2	Q8MQA1_CAEEL	q8mqa1 caenorhabd
559	76	6.4	2009	2	Q7R8P2_PLAYO	q7r8p2 plasmodium
560	76	6.4	3010	2	P90191_9HEPC	p90191 hepatitis c
561	76	6.4	3010	2	P90193_9HEPC	p90193 hepatitis c
562	76	6.4	3010	2	P90194_9HEPC	p90194 hepatitis c
563	75.5	6.4	156	1	MTR1A_RAT	mtr1a rattus norv
564	75.5	6.4	162	2	Q66PG7_XENLA	q66pg7 xenopus lae
565	75.5	6.3	206	2	Q6HMF5_BACHK	q6hmf5 bacillus th
566	75.5	6.3	220	2	Q61TR8_CAEBR	q61tr8 caenorhabdi
567	75.5	6.3	228	2	Q633A3_BACCZ	q633a3 bacillus ce
568	75.5	6.3	231	2	Q9VUN8_DROME	q9vun8 drosophila
569	75.5	6.3	244	2	Q6MD11_PARUW	q6md11 parachlamyd
570	75.5	6.3	247	2	Q7TPI3_RAT	q7tpi3 rattus norv
571	75.5	6.3	248	2	Q6HMF5_BACHK	q6hmf5 bacillus th
572	75.5	6.3	248	2	Q81YU8_BACAN	q81yu8 bacillus an
573	75.5	6.3	263	2	Q63GB2_BACCZ	q63gb2 bacillus ce
574	75.5	6.3	263	2	Q97PD2_STRPN	q97pd2 streptococc
575	75.5	6.3	263	2	Q9ESJ3_RAT	q9esj3 rattus norv
576	75.5	6.3	263	2	Q870H5_YEAST	q870h5 saccharomyc
577	75.5	6.3	266	2	Q4S7PI_TETNG	q4s7pi tetraodon n
578	75.5	6.3	269	2	Q5IPF7_9RODE	q5ipf7 perognathus
579	75.5	6.3	278	2	Q66PG6_XENLA	q66pg6 xenopus lae
580	75.5	6.3	301	2	Q865K7_MACEU	q865k7 macropus eu
581	75.5	6.3	301	2	Q5C281_SCHJA	q5c281 schistosoma
582	75.5	6.3	303	2	Q9KZ08_STRCO	q9kz08 streptomyce
583	75.5	6.3	305	2	Q4S7PI_TETNG	q4s7pi tetraodon n
584	75.5	6.3	310	2	Q870H5_YEAST	q870h5 saccharomyc
585	75.5	6.3	326	2	Q9ESJ3_RAT	q9esj3 rattus norv
586	75.5	6.3	339	2	Q9KSB3_VIBCH	q9ksb3 vibrio chol
587	75.5	6.3	342	2	Q59TA5_CANAL	q59ta5 candida alb
588	75.5	6.3	342	2	Q9QEV3_HHV8	q9qev3 human herpe
589	75.5	6.3	352	1	RNFD_ECO57	rnfd eco57
590	75.5	6.3	352	2	P58325_ECOLI	p58325 escherichia
591	75.5	6.3	352	2	P76182_ECOLI	p76182 escherichia
592	75.5	6.3	352	2	Q8FH94_ECOL6	q8fh94 escherichia
593	75.5	6.3	377	2	Q83KY5_SHIFL	q83ky5 shigella fl
594	75.5	6.3	379	1	CYB_ZAPTR	cyb zapus trino
595	75.5	6.3	379	2	Q4R2L1_VARHI	q4r2l1 varecula hi
596	75.5	6.3	389	2	Q50BJ8_PERFA	q50bj8 perognathus
597	75.5	6.3	397	2	Q8AYS5_HYLJA	q8ays5 hyla japoni
598	75.5	6.3	397	2	Q9N4R5_CAEEL	q9n4r5 caenorhabdi
599	75.5	6.3	400	2	Q6RXC2_HCMV	q6rxc2 human cytom
600	75.5	6.3	410	2	Q70NW4_9BILA	q70nw4 strongyloid
601	75.5	6.3	413	2	Q5UET7_ECOLI	q5uet7 escherichia
602	75.5	6.3	415	2	Q8XB33_ECOLI	q8xb33 escherichia
603	75.5	6.3	415	1	TNAB_ECOLI	tnab escherichia
604	75.5	6.3	415	1	TNAB_ECO57	tnab eco57
605	75.5	6.3	415	2	P23173_ECOLI	p23173 escherichia
606	75.5	6.3	430	2	Q5X337_LEGPA	q5x337 legionella
607	75.5	6.3	433	2	Q6F3C9_CAEEL	q6f3c9 caenorhabdi
608	75.5	6.3	446	2	Q7S8U0_NEUCR	q7s8u0 neurospora
609	75.5	6.3	466	2	Q4Y729_PLACH	q4y729 plasmodium
610	75.5	6.3	471	1	5HT2A_MOUSE	5ht2a mus musculu
611	75.5	6.3	471	2	P35363_MOUSE	p35363 mus musculu
612	75.5	6.3	481	2	Q543D4_MOUSE	q543d4 mus musculu
613	75.5	6.3	482	2	Q8COK0_MOUSE	q8cok0 mus musculu
614	75.5	6.3	491	2	Q9P6J0_SCHPO	q9p6j0 schizosacch
615	75.5	6.3	491	2	Q6SWJ1_HCMV	q6swj1 human cytom
	75.5	6.3	491	2	Q6SWS4_HCMV	q6sws4 human cytom
616	75.5	6.3	491	2	Q6SWV2_HCMV	q6swv2 human cytom
617	75.5	6.3	491	2	Q6SWY1_HCMV	q6swy1 human cytom
618	75.5	6.3	498	2	O47543_CHLEU	o47543 chlamydomon
619	75.5	6.3	501	2	Q6CHZ5_YARLI	q6chz5 yarrowia li
620	75.5	6.3	539	2	Q5CI52_CRYHO	q5ci52 cryptospori
621	75.5	6.3	551	2	FLVC2_MOUSE	flvc2 mus musculu
622	75.5	6.3	593	2	Q91X85_MOUSE	q91x85 mus musculu
623	75.5	6.3	593	2	Q25322_HELPY	q25322 helicobacte
624	75.5	6.3	708	2	Q5ZLM5_CHICK	q5zlm5 gallus gall
625	75.5	6.3	746	2	Q22806_CAEEL	q22806 caenorhabdi
626	75.5	6.3	773	2	Q8PGM4_XANAC	q8pgm4 xanthomonas
627	75.5	6.3	773	1	Q96325_ARATH	q96325 arabidopsis
628	75.5	6.3	795	1	CLCA_ARATH	clca arabidopsis
629	75.5	6.3	858	2	O61FT6_CAEBR	o61ft6 caenorhabdi
630	75.5	6.3	939	2	Q52B43_MAGGR	q52b43 magnaporthe
631	75.5	6.3	1008	2	Q5BG34_EMENI	q5bg34 aspergillus
632	75.5	6.3	1088	2	O89154_9HEPC	o89154 hepatitis c
633	75.5	6.3	1142	2	Q4UI92_THEAN	q4ui92 theileria
634	75.5	6.3	1583	2	Q9UT41_SCHPO	q9ut41 schizosach
635	75.5	6.3	3010	2	Q7P9S4_RICSI	q7p9s4 ricksettsia
636	75.5	6.3	3010	2	Q9J3G7_9HEPC	q9j3g7 hepatitis c
637	75.5	6.3	105	2	Q5AM04_CANAL	q5am04 candida alb
638	75.5	6.3	132	2	Q6N505_RHOPA	q6n505 rhodopseudo
639	75.5	6.3	152	2	Q4TPK6_9SPHN	q4tpk6 erythrobact
640	75.5	6.3	156	2	Q5FF13_EHRRG	q5ff13 ehrlichia r
641	75.5	6.3	156	2	Q4L9S9_STAHJ	q4l9s9 staphyloco
642	75.5	6.3	156	2	Q4L9S9_9CORO	q4l9s9 avian infec
643	75.5	6.3	170	2	Q81498_9HEPC	q81498 hepatitis c
644	75.5	6.3	215	2	Q81507_9HEPC	q81507 hepatitis c
645	75.5	6.3	218	2	Q81531_9HEPC	q81531 hepatitis c
646	75.5	6.3	220	2	Q4Y7N2_PLACH	q4y7n2 plasmodium
647	75.5	6.3	220	2	O34238_CAPSU	o34238 capricornis
648	75.5	6.3	227	2	Q6SKB1_ARTAU	q6skb1 arthrobacter
649	75.5	6.3	228	2	O63IU3_BACCZ	o63iu3 bacillus ce
650	75.5	6.3	256	2	Q631U3_BACCZ	q631u3 bacillus ce
651	75.5	6.3	274	2	Q9KNDO_VIBCH	q9knd0 vibrio chol
652	75.5	6.3	294	2	Q6MN43_BDEBA	q6mn43 bdellovibri
653	75.5	6.3	302	2	Q8RET4_FUSNN	q8ret4 fusobacteri
654	75.5	6.3	311	2	Q7NRF5_CHRVO	q7nrf5 chromobacte
655	75.5	6.3	318	2	Q6CVK2_KLULA	q6cvk2 kluyveromyc
656	75.5	6.3	330	2	Q52LG8_KLULA	q52lg8 kluyveromyc
657	75.5	6.3	371	2	Q4SMC3_TETNG	q4smc3 tetraodon n
658	75.5	6.3	373	2	Q58239_PYRHO	q58239 pyrococcus
659	75.5	6.3	380	1	Q8BW45_MOUSE	q8bw45 mus musculu
660	75.5	6.3	387	1	Y1368_METJA	y1368 metja
661	75.5	6.3	407	2	Q4YQG6_PLABE	q4yqg6 plasmodium
662	75.5	6.3	418	2	Q9GAT3_OCHHY	q9gat3 ochotona hy
663	75.5	6.3	418	2	Q6VMD0_9CORO	q6vmd0 9coro
664	75.5	6.3	418	2	Q6A8T1_PROAC	q6a8t1 propionibac
665	75.5	6.3	424	2	Q6QFB8_LEGPN	q6qfb8 legionella
666	75.5	6.3	425	2	Q5WZ83_LEGPL	q5wz83 legionella
667	75.5	6.3	460	2	Q5X7T2_LEGPA	q5x7t2 legionella
668	75.5	6.3	460	2	Q4TP70_9SPHN	q4tp70 erythrobact
669	75.5	6.3	473	2	Q4Z7S9_9SPHN	q4z7s9 erythrobact
670	75.5	6.3	473	2	Q427S9_PLABE	q427s9 plasmodium
671	75.5	6.3	488	2	Q63QA3_BURPS	q63qa3 burkholderi
672	75.5	6.3	498	2	Q62GF6_BURMA	q62gf6 burkholderi
673	75.5	6.3	526	2	P24046_HUMAN	p24046 burkholderi
674	75.5	6.3	543	1	GBRR1_HUMAN	gbrr1 human
675	75.5	6.3	625	2	Q9BX06_HUMAN	q9bx06 homo sapien
676	75.5	6.3	649	2	Q7RW58_NEUCR	q7rw58 neurospora
677	75.5	6.3	662	2	Q7SU67_FUGRU	q7su67 fugu rubrip
678	75.5	6.3	753	2	Q9SN21_ARATH	q9sn21 arabidopsis
679	75.5	6.3	777	2	Q7NS50_CHRVO	q7ns50 chromobacte
680	75	6.3	838	1	KIP2_LEGPH	kip2 legionella
681	75	6.3	883	2	Q34952_BACSU	q34952 bacillus su
682	75	6.3	883	2	Q7VED4_PROMA	q7ved4 prochloroco
683	75	6.3	937	2	Q98S90_GUITH	q98s90 guillardia
684	75	6.3	662	2	Q6BG55_PARTE	q6bg55 paramecium
685	75	6.3	753	2	Q4HZA9_GIBZE	q4hza9 gibberella
686	75	6.3	777	2	Q4N412_THEPA	q4n412 theileria p
687	75	6.3	937	2	Q82ZR7_METMA	q82zr7 methanosarc
688	75	6.3	1008	2	O89153_9HEPC	o89153 hepatitis c

No.			Len	n	Accession	Organism
689	75	6.3	1008	2	O89156_9HEPC	hepatitis c
690	75	6.3	1008	2	O89152_9HEPC	hepatitis c
691	75	6.3	1131	2	Q8NAT5_HUMAN	homo sapien
692	75	6.3	1145	2	Q8GUE7_9LILI	cymodocea n
693	75	6.3	1154	2	Q6FTI6_CANGA	candida gla
694	75	6.3	1336	2	Q6F1I1_MESFL	mesoplasma
695	75	6.3	1704	2	Q95206_9TRYP	trypanosoma
696	75	6.3	2248	1	P32870_DROME	drosophila
697	75	6.3	2846	2	CYA1_DICDI	dictyosteli
698	75	6.3	3010	2	Q68833_9HEPC	hepatitis c
699	75	6.3	3010	2	Q9J3G2_9HEPC	hepatitis c
700	75	6.3	3010	2	Q9J3G5_9HEPC	hepatitis c
701	75	6.3	3010	2	Q9QIY7_9HEPC	hepatitis c
702	75	6.3	3010	2	Q9QIY8_9HEPC	hepatitis c
703	74.5	6.2	174	2	P97068_9ENTR	salmonella
704	74.5	6.2	179	2	Q8EPH9_OCEIH	oceanobacil
705	74.5	6.2	180	2	P71253_ECOLI	escherichia
706	74.5	6.2	227	2	Q9GAT5_OCHTI	ochotona th
707	74.5	6.2	227	2	Q9GAT4_OCHCU	ochotona cu
708	74.5	6.2	227	2	Q9GAT6_OCHPR	ochotona pr
709	74.5	6.2	258	2	Q88WC7_LACPL	lactobacill
710	74.5	6.2	276	2	Q9R9Q5_RHIME	rhizobium m
711	74.5	6.2	280	2	Q6WIF6_SYNP8	synechococc
712	74.5	6.2	290	2	Q6SEU1_9BACT	uncultured
713	74.5	6.2	290	2	Q6BWD3_DEBHA	debaryomyce
714	74.5	6.2	298	2	Q51EN3_ENTHI	entamoeba h
715	74.5	6.2	298	2	Q8R7K6_THETN	thermoanaer
716	74.5	6.2	313	2	Q9WX57_THEMA	thermotoga
717	74.5	6.2	335	2	Q5FMX7_LACAC	lactobacill
718	74.5	6.2	346	2	P49238_CX3C1_HUMAN	homo sapien
719	74.5	6.2	355	1	O5WHM9_BACSK	bacillus cl
720	74.5	6.2	358	2	O8IDY2_PLAF7	plasmodium
721	74.5	6.2	364	2	O766W3_VARHI	vargula hil
722	74.5	6.2	377	2	Q4R2N5_VARHI	vargula hil
723	74.5	6.2	377	2	Q4R2N4_VARHI	vargula hil
724	74.5	6.2	377	2	Q4R2K8_VARHI	vargula hil
725	74.5	6.2	377	2	Q4R2K5_VARHI	vargula hil
726	74.5	6.2	377	2	Q4R2K3_VARHI	vargula hil
727	74.5	6.2	377	2	Q4R2K2_VARHI	vargula hil
728	74.5	6.2	377	2	Q4R2K1_VARHI	vargula hil
729	74.5	6.2	377	2	Q4R2J3_VARHI	vargula hil
730	74.5	6.2	377	2	Q4R2I1_VARHI	vargula hil
731	74.5	6.2	377	2	Q4R2H9_VARHI	vargula hil
732	74.5	6.2	377	2	Q4R2H6_VARHI	vargula hil
733	74.5	6.2	377	2	Q4R2G0_VARHI	vargula hil
734	74.5	6.2	377	2	Q4R2F7_VARHI	vargula hil
735	74.5	6.2	377	2	Q4R2B4_VARHI	vargula hil
736	74.5	6.2	377	2	Q4R2C4_VARHI	vargula hil
737	74.5	6.2	377	2	Q4R2C9_VARHI	vargula hil
738	74.5	6.2	377	2	Q4R2D6_VARHI	vargula hil
739	74.5	6.2	377	2	Q4R2E3_VARHI	vargula hil
740	74.5	6.2	377	2	Q4R2D8_VARHI	vargula hil
741	74.5	6.2	377	2	Q4R2E6_VARHI	vargula hil
742	74.5	6.2	377	2	Q4R2E5_VARHI	vargula hil
743	74.5	6.2	377	2	Q4R2C3_VARHI	vargula hil
744	74.5	6.2	377	2	Q4R296_VARHI	vargula hil
745	74.5	6.2	377	2	Q4R295_VARHI	vargula hil
746	74.5	6.2	377	2	Q4R290_VARHI	vargula hil
747	74.5	6.2	377	2	Q4R289_VARHI	vargula hil
748	74.5	6.2	377	2	Q4R288_VARHI	vargula hil
749	74.5	6.2	377	2	Q4R286_VARHI	vargula hil
750	74.5	6.2	377	2	Q4R285_VARHI	vargula hil
751	74.5	6.2	377	2	Q4R273_VARHI	vargula hil
752	74.5	6.2	377	2	Q4R268_VARHI	vargula hil
753	74.5	6.2	377	2	Q4R1Z4_VARHI	vargula hil
754	74.5	6.2	377	2	Q4R1Z6_VARHI	vargula hil
755	74.5	6.2	377	2	Q4R1Z8_VARHI	vargula hil
756	74.5	6.2	377	2	Q4R1Y1_VARHI	vargula hil
757	74.5	6.2	377	2	Q4R1X3_VARHI	vargula hil
758	74.5	6.2	377	2	Q4R1W3_VARHI	vargula hil
759	74.5	6.2	377	2	Q4R1V6_VARHI	vargula hil
760	74.5	6.2	377	2	Q4R1V6_VARHI	vargula hil
761	74.5	6.2	377	2	Q4R1V6_VARHI	vargula hil
762	74.5	6.2	377	2	Q4R1V3_VARHI	vargula hil
763	74.5	6.2	377	2	Q4R1V2_VARHI	vargula hil
764	74.5	6.2	377	2	Q4R2N2_VARHI	vargula hil
765	74.5	6.2	377	2	Q4R2N1_VARHI	vargula hil
766	74.5	6.2	377	2	Q4R2N6_VARHI	vargula hil
767	74.5	6.2	377	2	Q4R2E4_VARHI	vargula hil
768	74.5	6.2	377	2	Q4R2G6_VARHI	vargula hil
769	74.5	6.2	377	2	Q4R2E9_VARHI	vargula hil
770	74.5	6.2	377	2	Q4R294_VARHI	vargula hil
771	74.5	6.2	377	2	Q4R292_VARHI	vargula hil
772	74.5	6.2	377	2	Q4R2M1_VARHI	vargula hil
773	74.5	6.2	377	2	Q4R2A2_VARHI	vargula hil
774	74.5	6.2	377	2	Q4R2E7_VARHI	vargula hil
775	74.5	6.2	377	2	Q4R1Y8_VARHI	vargula hil
776	74.5	6.2	377	2	Q4R1Y9_VARHI	vargula hil
777	74.5	6.2	377	2	Q4R2M8_VARHI	vargula hil
778	74.5	6.2	377	2	Q4R2P2_VARHI	vargula hil
779	74.5	6.2	378	1	Q6DUV8_BRANA	brassica na
780	74.5	6.2	379	2	Q6ELW8_OCHPR	ochotona pr
781	74.5	6.2	379	2	Q6ELW8_OCHPR	ochotona pr
782	74.5	6.2	379	2	Q8WB05_APLRU	aplodontia
783	74.5	6.2	379	2	Q8WB05_CHAPN	chaetodipus
784	74.5	6.2	379	2	Q9B9E3_CHAPN	chaetodipus
785	74.5	6.2	379	2	Q91CN4_MICOL	micromonosp
786	74.5	6.2	379	2	Q94AI3_ARATH	arabidopsis
787	74.5	6.2	379	1	Q94AI3_ARATH	arabidopsis
788	74.5	6.2	392	2	Q5Y9V2_CANAL	candida alb
789	74.5	6.2	442	2	Q5Y9V2_CANAL	candida alb
790	74.5	6.2	450	2	Q65MD8_BACLD	bacillus li
791	74.5	6.2	450	1	P14842_5HT2A_RAT	rattus norv
792	74.5	6.2	458	2	Q4U3W9_MESAU	mesocricetu
793	74.5	6.2	471	2	Q9K5Y9_BACHD	bacillus ha
794	74.5	6.2	473	2	Q6QU71_ASPTU	aspergillus
795	74.5	6.2	471	1	O24348_SORBI	sorghum bic
796	74.5	6.2	488	2	Q55UE4_SORBI	sorghum bic
797	74.5	6.2	488	2	Q5KI02_CRYNE	cryptococcu
798	74.5	6.2	500	2	Q5KI02_CRYNE	cryptococcu
799	74.5	6.2	523	2	Q66GQ5_MAGGR	magnaporthe
800	74.5	6.2	523	2	Q52ER6_MAGGR	magnaporthe
801	74.5	6.2	540	2	Q8N2S3_HUMAN	homo sapien
802	74.5	6.2	548	2	O22454_WHEAT	triticum ae
803	74.5	6.2	562	2	Q4WLQ1_ASPFU	aspergillus
804	74.5	6.2	574	2	Q9VD40_DROME	drosophila
805	74.5	6.2	594	2	P36029_USTMA	ustilago ma
806	74.5	6.2	597	2	Q8VVK9_CORGL	corynebacte
807	74.5	6.2	618	1	Q8D8M2_VIBVU	vibrio vuln
808	74.5	6.2	793	2	Q4U8N7_THEAN	theileria a
809	74.5	6.2	848	2	Q7Z2C1_TRYBB	trypanosoma
810	74.5	6.2	990	1	Q7Z2C0_TRYPA	trypanosoma
811	74.5	6.2	1022	2	Q94447_CALVI	calliphora
812	74.5	6.2	1033	2	Q61PW5_CAEBR	caenorhabdi
813	74.5	6.2	1034	2	Q7S0S1_NEUCR	neurospora
814	74.5	6.2	1183	2	Q54Z25_DICDI	dictyosteli
815	74.5	6.2	1534	2	Q54TV1_DICDI	dictyosteli
816	74.5	6.2	1520	2	Q8T687_DICDI	dictyosteli
817	74.5	6.2	1808	2	O81KF1_PLAF7	plasmodium
818	74	6.2	1837	2	Q91AU0_9HEPC	hepatitis c
819	74	6.2	3010	2	O81528_9HEPC	hepatitis c
820	74	6.2	124	2	Q8KC46_CHLTE	chlorobium
821	74	6.2	156	2	O8WZ72_HUMAN	homo sapien
822	74	6.2	167	2	Q5VHX0_EAV	equine arte
823	74	6.2	173	1	Q5HCD2_EHRRW	ehrlichia r
824	74	6.2	220	2	Q91SA2_9CORO	avian infec
825	74	6.2	225	1	O88Y70_LACPL	lactobacill
826	74	6.2	230	2	O27961_ARCFU	archaeoglob
827	74	6.2	231	2	O28892_ARCFU	archaeoglob
828	74	6.2	238	2	Q6HET1_BACHK	bacillus th
829	74	6.2	255	2	Q66483_EAV	equine arte
830	74	6.2	278	2	Q6CUI8_KLULA	kluyveromyc
831	74	6.2	286	1	Q4XPR5_PLACH	plasmodium
832	74	6.2	291	1	P75058_POTB_MYCPN	mycoplasma
833	74	6.2	295	2	Q66GG8_YERPS	yersinia ps
834	74	6.2	295	1	Q9WWR5_CYOE_PSEPU	pseudomonas
			297	2	Q64M3_PSEPU	pseudomonas
			300	2	Q61BC3_CAEBR	caenorhabdi
				1	P24877_N2M_ASCSU	ascaris suu

No.	S1	S2	Len	Ch	Accession	Organism
835	74	6.2	312	1	PYRB_AERPE	q9ybd4 aeropyrum p
836	74	6.2	312	2	Q9CH74_LACLA	q9ch74 lactococcus
837	74	6.2	315	2	Q710S2_SPAEH	q710s2 spalax leuc
838	74	6.2	321	2	Q8M6V0_9MAXI	q8m6v0 tigriopus j
839	74	6.2	324	2	Q8DVZ6_STRMU	q8dvz6 streptococc
840	74	6.2	333	2	Q4FN51_9RICK	q4fn51 candidatus
841	74	6.2	339	2	Q61FG9_CAEBR	q61fg9 caenorhabdi
842	74	6.2	342	2	Q621V1_CAEBR	q621v1 caenorhabdi
843	74	6.2	349	1	I10R2_MOUSE	i10r2 mus musculu
844	74	6.2	350	1	P48039_MOUSE	p48039 mus musculu
845	74	6.2	351	2	Q8VHM7_MOUSE	q8vhm7 mus musculu
846	74	6.2	354	2	Q65U34_MANSM	q65u34 mannheimia
847	74	6.2	357	2	Q5FV66_MEDTR	q5fv66 medicago tr
848	74	6.2	361	2	Q64AL9_9ARCH	q64al9 uncultured
849	74	6.2	379	1	CYB_THOMO	q8wek2 thomomys mo
850	74	6.2	379	2	Q48002_THOMO	q48002 thomomys mo
851	74	6.2	379	2	Q48902_THOMO	q48902 thomomys mo
852	74	6.2	379	2	Q48003_THOMO	q48003 thomomys mo
853	74	6.2	379	2	Q47980_THOBO	q47980 thomomys bo
854	74	6.2	379	2	Q8WEK5_THOTA	q8wek5 thomomys ta
855	74	6.2	379	2	Q8HHJ7_THOBO	q8hhj7 thomomys bo
856	74	6.2	379	2	Q59JJ7_9SCIU	q59jj7 thomomys vo
857	74	6.2	380	1	Q74KB0_LACCO	q74kb0 lactobacill
858	74	6.2	381	1	CYB_PSENI	q35553 pseudantech
859	74	6.2	382	2	Q5R7A1_PONPY	q5r7a1 pongo pygma
860	74	6.2	396	2	Q6GAR1_STAAS	q6gar1 staphylococ
861	74	6.2	396	2	Q6G168_STAAR	q6g168 staphylococ
862	74	6.2	396	2	Q5HH70_STAAC	q5hh70 staphylococ
863	74	6.2	396	2	Q7A6D3_STAAN	q7a6d3 staphylococ
864	74	6.2	396	2	Q8NXC4_STAAW	q8nxc4 staphylococ
865	74	6.2	397	2	Q99V76_STAAM	q99v76 staphylococ
866	74	6.2	398	2	Q42Z54_PLABE	q42z54 plasmodium
867	74	6.2	410	2	Q5NEU8_FRATT	q5neu8 francisella
868	74	6.2	418	2	Q4RIO3_TETNG	q4rio3 tetraodon n
869	74	6.2	418	2	Q6FBF9_LEGPN	q6fbf9 legionella
870	74	6.2	418	2	Q6FC5_LEGPN	q6fc5 legionella
871	74	6.2	436	2	Q6QFC7_LEGPN	q6qfc7 legionella
872	74	6.2	442	2	Q5QZG8_IDILO	q5qzg8 idiomarina
873	74	6.2	452	2	Q9CEG6_LACLA	q9ceg6 lactococcus
874	74	6.2	457	2	Q4NJC7_9MICC	q4njc7 arthrobacte
875	74	6.2	475	2	Q8RBZ7_THETN	q8rbz7 thermoanaer
876	74	6.2	481	2	Q9S2G7_STRCO	q9s2g7 streptomyce
877	74	6.2	481	2	Q4Q1F4_LEIMA	q4q1f4 leishmania
878	74	6.2	485	2	Q9XVK0_CAEEL	q9xvk0 caenorhabdi
879	74	6.2	487	2	O23384_ARATH	o23384 arabidopsis
880	74	6.2	493	2	Q42254_PLABE	q42254 arabidopsis
881	74	6.2	503	2	Q6M052_METMP	q6m052 methanococc
882	74	6.2	505	2	Q4NS89_9DELT	q4ns89 anaeromyxob
883	74	6.2	528	2	Q70109_KLULA	q70109 kluyveromyc
884	74	6.2	530	2	Q5IFL8_ENTHI	q5ifl8 entamoeba h
885	74	6.2	540	2	Q6LF33_PLAF7	q6lf33 plasmodium
886	74	6.2	581	2	Q5KA08_CRYNE	q5ka08 cryptococcu
887	74	6.2	584	2	Q5KA09_CRYNE	q5ka09 cryptococcu
888	74	6.2	599	2	Q9S6S6_9LACT	q9s6s6 lactococcus
889	74	6.2	650	2	Q4FTS7_9GAMM	q4fts7 psychrobact
890	74	6.2	681	2	Q6FNV6_CANGA	q6fnv6 candida gla
891	74	6.2	742	2	Q9AIP1_CARRU	q9aip1 carsonella
892	74	6.2	841	2	Q9AIP1_CARRU	q9aip1 carsonella
893	74	6.2	846	2	Q93U47_CARRU	q93u47 carsonella
894	74	6.2	892	2	Q8TGB2_CANAL	q8tgb2 candida alb
895	74	6.2	943	2	Q4IMI9_GIBZE	q4imi9 gibberella
896	74	6.2	1123	2	Q9SE99_ARATH	q9se99 arabidopsis
897	74	6.2	1123	2	Q9SPU7_ARATH	q9spu7 arabidopsis
898	74	6.2	1216	2	Q55IS2_CRYNE	q55is2 cryptococcu
899	74	6.2	1216	2	Q5KCX7_CRYNE	q5kcx7 cryptococcu
900	74	6.2	3010	2	Q913V3_9HEPC	q913v3 hepatitis c
901	74	6.2	3010	2	Q9DTE8_9HEPC	q9dte8 hepatitis c
902	74	6.2	3010	2	Q93H6_9HEPC	q93h6 hepatitis c
903	74	6.2	3010	2	Q9QIY1_9HEPC	q9qiy1 hepatitis c
904	74	6.2	120	2	Q9QIY2_9HEPC	q9qiy2 hepatitis c
905	73.5	6.2	153	2	Q9SKA6_ARATH	q9ska6 arabidopsis
906	73.5	6.2	180	2	Q92XD3_RHIME	q92xd3 rhizobium m
907	73.5	6.2	180	2	Q82XS3_PYRAE	q82xs3 pyrobaculum
908	73.5	6.2	180	2	P71257_ECOLI	p71257 escherichia
909	73.5	6.2	180	2	P75018_ECOLI	p75018 escherichia
910	73.5	6.2	199	2	Q8DVR3_STRMU	q8dvr3 streptococc
911	73.5	6.2	216	1	Y2036_AQUAE	y2036 aquifex aeo
912	73.5	6.2	217	2	O67827_AQUAE	o67827 aquifex aeo
913	73.5	6.2	226	2	Q4TEY9_TETNG	q4tey9 tetraodon n
914	73.5	6.2	226	2	Q5MAP0_9CORO	q5map0 avian infec
915	73.5	6.2	226	1	Q9J0X1_9CORO	q9j0x1 avian infec
916	73.5	6.2	267	2	Q50Z61_ENTHI	q50z61 entamoeba h
917	73.5	6.2	270	2	Q8HIY6_PERLO	q8hiy6 perognathus
918	73.5	6.2	270	2	Q8HBP0_PERLO	q8hbp0 perognathus
919	73.5	6.2	274	2	Q8HIY6_PERIO	q8hiy6 perognathus
920	73.5	6.2	278	2	Q4HS16_CAMUP	q4hs16 campylobact
921	73.5	6.2	286	2	Q6Z2T3_ORYSA	q6z2t3 oryza sativ
922	73.5	6.2	296	2	Q5J3K6_RAT	q5j3k6 rattus norv
923	73.5	6.2	303	2	Q5NP42_ZYMMO	q5np42 zymomonas m
924	73.5	6.2	304	2	Q4PO66_USTMA	q4po66 ustilago ma
925	73.5	6.2	318	2	Q588N8_SCILI	q588n8 sciurus lis
926	73.5	6.2	338	1	Q5S895_SYNY3	q5s895 synechocyst
927	73.5	6.2	355	2	YAD_BACSU	p37520 bacillus su
928	73.5	6.2	360	2	Q4J826_SULAC	q4j826 sulfolobus
929	73.5	6.2	367	2	Q50810_9RODE	q50810 perognathus
930	73.5	6.2	373	2	P15547_STRPU	p15547 strongyloce
931	73.5	6.2	379	1	CYB_BRARE	q8uuw8 brachydanio
932	73.5	6.2	379	1	Q8UUW8_BRARE	q8uuw8 uncultured
933	73.5	6.2	379	2	Q64BD6_9ARCH	q64bd6 uncultured
934	73.5	6.2	380	1	Q64BD6_9ARCH	q64bd6 salmonella
935	73.5	6.2	384	2	Q5F117_LACAC	q5f117 salmonella
936	73.5	6.2	384	1	CYB_PHOGR	q35457 lactobacill
937	73.5	6.2	385	2	Q35457_PHOCA	q35457 phoca green
938	73.5	6.2	387	2	CYB_THOTA	q2z719 thomomys
939	73.5	6.2	387	2	Q82G27_SALTI	q82g27 salmonella
940	73.5	6.2	389	1	Q9KWU2_9SPHN	q9kwu2 sphingomona
941	73.5	6.2	391	2	Q7MVX5_PORGI	q7mvx5 porphyromon
942	73.5	6.2	391	1	P56494_MACMU	p56494 macaca mula
943	73.5	6.2	409	2	P56449_BOVIN	p56449 bos taurus
944	73.5	6.2	413	2	Q82ZF7_ENTFA	q82zf7 enterococcu
945	73.5	6.2	421	2	Q7V140_PROMP	q7v140 prochloroco
946	73.5	6.2	425	2	Q928T3_LISIN	q928t3 listeria in
947	73.5	6.2	442	2	Q8PK37_XANAC	q8pk37 xanthomonas
948	73.5	6.2	442	2	Q6D6K1_ERWCT	q6d6k1 erwinia car
949	73.5	6.2	491	1	Q8GZ34_ARATH	q8gz34 arabidopsis
950	73.5	6.2	491	2	Q9XIQ7_ARATH	q9xiq7 arabidopsis
951	73.5	6.2	491	1	P13202_HCMVA	p13202 human cytom
952	73.5	6.2	518	2	O6SW28_HCMV	o6sw28 human cytom
953	73.5	6.2	523	2	Q7RT44_PLAYO	q7rt44 plasmodium
954	73.5	6.2	542	2	Q64WY6_BACFR	q64wy6 bacteroides
955	73.5	6.2	557	2	Q5LG29_BACFN	q5lg29 bacteroides
956	73.5	6.2	563	2	Q7PFV1_ANOGA	q7pfv1 anopheles g
957	73.5	6.2	574	2	Q8VZE2_ARATH	q8vze2 arabidopsis
958	73.5	6.2	574	2	Q5ATP6_EMENI	q5atp6 arabidopsis
959	73.5	6.2	607	2	Q93990_CANAL	q93990 aspergillus
960	73.5	6.2	614	2	Q6DFJ5_XENLA	q6dfj5 arabidopsis
961	73.5	6.2	634	1	Q5A4P9_CANAL	q5a4p9 xenopus lae
962	73.5	6.2	637	2	Q5CE41_CRYHO	q5ce41 candida alb
963	73.5	6.2	640	1	Q9PC78_XYLFA	q9pc78 cryptospori
964	73.5	6.2	653	2	Q9KACL_BACHD	q9kacl xylella fas
965	73.5	6.2	661	2	MUTL_BACHD	mutl bacillus ha
966	73.5	6.2	731	2	APRN_ENTHI	aprn entamoeba h
967	73.5	6.2	846	2	P20301_METAC	p20301 methanosarc
968	73.5	6.2	859	2	Q8TTH1_METAC	q8tth1 corynebacte
969	73.5	6.2	881	2	Q68468_CORAM	q68468 glyceria gr
970	73.5	6.2	992	2	Q5IWR5_GLYGR	q5iwr5 caenorhabdi
971	73.5	6.2	1006	2	O16531_CAEEL	o16531 carsonella
972	73.5	6.2	1049	2	Q4YQY1_PLABE	q4yqy1 plasmodium
973	73.5	6.2	1095	2	Q5ZM00_CHICK	q5zm00 gallus gall
974	73.5	6.2	1174	2	Q5I3I5_ENTHI	q5i3i5 plasmodium
975	73.5	6.2	1175	2	Q4YH96_PLABE	q4yh96 entamoeba h
976	73.5	6.2	1277	2	Q6FTY2_CANGA	q6fty2 candida gla
977	73.5	6.2	—	2	Q9C7H5_ARATH	q9c7h5 plasmodium
978	73.5	6.2	—	2	Q7M006_9CORO	q7m006 arabidopsis
979	73.5	6.2	—	2	Q4HDG2_CAMCO	q4hdg2 murine hepa
980	73.5	6.2	—	2	Q76G00_CIOIN	q76g00 ciona intes

#	score1	score2	length	n	accession	organism
981	73.5	6.2	1287	2	Q7YU59_DROME	drosophila
982	73.5	6.2	1287	2	Q9U5W1_DROME	drosophila
983	73.5	6.2	1292	2	Q9VL24_DROME	drosophila
984	73.5	6.2	1292	2	Q9AIH0_CARRU	carsonella
985	73.5	6.2	1476	2	Q96SD3_DICDI	dictyosteli
986	73.5	6.2	1545	2	Q8GU65_ORYSA	oryza sativ
987	73.5	6.2	2666	2	Q6FW99_CANGA	candida gla
988	73.5	6.2	3007	2	Q4SSR8_TETNG	tetraodon n
989	73.5	6.2	3010	2	Q9DTE6_9HEPC	hepatitis c
990	73.5	6.2	3381	2	Q8IDK4_PLAF7	plasmodium
991	73.5	6.2	4470	2	R1AB_CVMA5	murine hepa
992	73.5	6.2	4470	2	Q66WN5_9CORO	murine hepa
993	73.5	6.2	7176	1	P16342	n replicase
994	73.5	6.2	7178	1	Q66WN6_9CORO	murine hepa
995	73	6.2	114	2	Q75XA7_HELPY	helicobacte
996	73	6.2	114	2	Q9ZLU2_HELPJ	helicobacte
997	73	6.1	138	2	O77777_ELEMA	elephas max
998	73	6.1	140	2	Q64145_9MURI	rattus sp.
999	73	6.1	145	2	Q9UXB0_SULSO	sulfolobus
1000	73	6.1	155	2	Q7VJP1_HELHP	helicobacte
1001	73	6.1	156	2	Q81510_9HEPC	hepatitis c
1002	73	6.1	156	2	Q81522_9HEPC	hepatitis c
1003	73	6.1	163	2	Q81537_9HEPC	hepatitis c
1004	73	6.1	220	2	Q80RY8_9CORO	avian infec
1005	73	6.1	220	2	O72Z40_BACC1	bacillus ce
1006	73	6.1	223	1	VME1_IBVG	avian infec
1007	73	6.1	223	2	Q91S97_9CORO	avian infec
1008	73	6.1	226	2	Q7T9P6_9CORO	avian infec
1009	73	6.1	238	2	O81986_BACCI	bacillus ce
1010	73	6.1	238	2	Q4MJ45_BACCE	bacillus ce
1011	73	6.1	238	2	Q636E3_BACCZ	bacillus ce
1012	73	6.1	249	2	Q732I6_BACC1	bacillus ce
1013	73	6.1	255	2	Q9FDU6_STRPY	streptococc
1014	73	6.1	255	2	P87639_EAV	equine arte
1015	73	6.1	260	2	Q9YNU0_EAV	equine arte
1016	73	6.1	264	2	Q7QN39_ANOGA	anopheles g
1017	73	6.1	264	2	Q8DAQ9_VIBVU	vibrio vuln
1018	73	6.1	279	2	Q7MJ52_VIBVY	vibrio vuln
1019	73	6.1	282	1	Q6TY95_9BILA	xiphinema a
1020	73	6.1	290	1	NU2M_CAEEL	caenorhabdi
1021	73	6.1	290	2	Q6G9W4_STAAS	staphylococ
1022	73	6.1	290	2	Q5HGI3_STAAC	staphylococ
1023	73	6.1	294	2	Q8NX00_STAAW	staphylococ
1024	73	6.1	294	2	Q4X7M3_PLACH	plasmodium
1025	73	6.1	295	2	Q4XT47_PLACH	plasmodium
1026	73	6.1	295	2	Q5AZG6_EMENI	aspergillus
1027	73	6.1	295	2	Q8VUQ2_PSEPU	pseudomonas
1028	73	6.1	303	2	Q88PN3_PSEPK	pseudomonas
1029	73	6.1	314	2	Q94EJ0_ARATH	arabidopsis
1030	73	6.1	322	2	Q8ESH3_OCEIH	oceanobacil
1031	73	6.1	326	2	Q99NR7_MUSAV	muscardinus
1032	73	6.1	335	2	Q8SWL8_ENCCU	encephalito
1033	73	6.1	339	1	P54129_CAEEL	caenorhabdi
1034	73	6.1	340	2	Q9N2T2_CAEEL	caenorhabdi
1035	73	6.1	343	2	Q7YFU0_9HYME	myrmica sul
1036	73	6.1	343	2	Q85AS7_UMASC	uma scopari
1037	73	6.1	348	2	Q9TD49_9SMEG	cynolebias
1038	73	6.1	364	1	Q99p50	mus musculu
1039	73	6.1	364	1	GHSR_MOUSE	mus musculu
1040	73	6.1	375	1	GHSR_RAT	rattus norv
1041	73	6.1	378	2	O86NC0_CAEEL	caenorhabdi
1042	73	6.1	378	2	Q70EG5_9RODE	saccostomus
1043	73	6.1	379	2	Q70EG4_9RODE	saccostomus
1044	73	6.1	379	2	Q8WDV7_CRATY	cratogeomys
1045	73	6.1	379	2	Q34099_CRAFU	cratogeomys
1046	73	6.1	379	2	Q69BQ2_CRAFU	cratogeomys
1047	73	6.1	383	2	Q9GL20_CYNSP	cynopterus
1048	73	6.1	391	2	Y450_BUCAP	buchnera ap
1049	73	6.1	394	1	Q6EE99_LATCH	latimeria c
1050	73	6.1	399	2	Q6L0J3_PICTO	picrophilus
1051	73	6.1	401	2	Q6KZX3_PICTO	picrophilus
1052	73	6.1	412	2	Q6lM38_CAEBR	caenorhabdi
1053	73	6.1	437	2	Q4YN50_PLABE	plasmodium
1054	73	6.1	446	2	Q8H9B3_BRACM	brassica ca
1055	73	6.1	450	1	VGLM_EH1B	equine herp
1056	73	6.1	450	1	P28948	equine herp
1057	73	6.1	453	2	Q6S6V2_9ALPH	equid herpe
1058	73	6.1	461	2	Q94307_CAEEL	caenorhabdi
1059	73	6.1	461	2	Q9R923_STRPN	streptococc
1060	73	6.1	470	2	Q4K0J6_STRPN	streptococc
1061	73	6.1	474	2	Q54PF0_DICDI	dictyosteli
1062	73	6.1	481	2	Q94CI7_ARATH	arabidopsis
1063	73	6.1	481	2	Q4K4Z1_PSEF5	pseudomonas
1064	73	6.1	487	2	Q7MBA5_PHOLL	photorhabdu
1065	73	6.1	488	2	Q4HRT1_CAMUP	campylobact
1066	73	6.1	494	1	KCNF1_HUMAN	homo sapien
1067	73	6.1	494	1	Q9H3M0	homo sapien
1068	73	6.1	509	2	Q58S13_HUMAN	homo sapien
1069	73	6.1	510	2	Q8N5L3_HUMAN	homo sapien
1070	73	6.1	520	2	Q27072_TAESO	taenia soli
1071	73	6.1	546	2	Q5CUK7_CRYPV	cryptospori
1072	73	6.1	546	2	Q5KWR7_GEOKA	geobacillus
1073	73	6.1	553	2	Q5EAY8_XENLA	xenopus lae
1074	73	6.1	553	2	Q59PN9_CANAL	candida alb
1075	73	6.1	556	2	Q92JJ5_HELPJ	helicobacte
1076	73	6.1	616	2	Q7QZJ9_GIALA	giardia lam
1077	73	6.1	623	2	Q6BIQ1_DEBHA	debaryomyce
1078	73	6.1	635	2	Q86X77_HUMAN	homo sapien
1079	73	6.1	643	2	Q4RMH4_TETNG	tetraodon n
1080	73	6.1	668	2	Q7NBK6_MYCGA	mycoplasma
1081	73	6.1	668	2	Q9ALX8_BURPS	burkholderi
1082	73	6.1	676	2	Q63L61_BURPS	burkholderi
1083	73	6.1	703	2	Q9VF31_DROME	drosophila
1084	73	6.1	716	1	Q4W5R5_CANAL	candida alb
1085	73	6.1	716	2	Q59LX3_CANAL	candida alb
1086	73	6.1	789	2	O82EJ8_ORYSA	oryza sativ
1087	73	6.1	792	2	Q5HGF5_STAAC	staphylococ
1088	73	6.1	832	2	Q7UQF9_RHOBA	rhodopirell
1089	73	6.1	844	2	Q6KYT8_PICTO	picrophilus
1090	73	6.1	861	1	Q9AVX8_GUITH	guillardia
1091	73	6.1	966	1	PK02_MOUSE	mus musculu
1092	73	6.1	966	1	Q8BPR6_MOUSE	mus musculu
1093	73	6.1	971	2	Q7TSI7_MOUSE	mus musculu
1094	73	6.1	1035	1	O60337_HUMAN	homo sapien
1095	73	6.1	1075	2	Q967W1_SCHMA	schistosoma
1096	73	6.1	1111	2	Q9LPE2_ARATH	arabidopsis
1097	73	6.1	1111	2	Q86FP2_CAEEL	caenorhabdi
1098	73	6.1	1127	2	Q9N323_CAEEL	caenorhabdi
1099	73	6.1	1156	2	Q4WGM4_ASPFU	aspergillus
1100	73	6.1	1268	2	Q53TS5_DICDI	dictyosteli
1101	73	6.1	1931	2	Q8RJY3_STIAU	stigmatella
1102	73	6.1	1951	2	Q7PZN7_ANOGA	anopheles g
1103	73	6.1	3010	2	P88803_9HEPC	hepatitis c
1104	73	6.1	3010	2	Q9J3G1_9HEPC	hepatitis c
1105	73	6.1	3010	2	Q9J3I0_9HEPC	hepatitis c
1106	73	6.1	3013	2	Q90IX9_9HEPC	hepatitis c
1107	73	6.1	3013	2	Q90IY0_9HEPC	hepatitis c
1108	73	6.1	6875	2	Q8R733_RABIT	oryctolagus
1109	72.5	6.1	105	2	Q5ALK7_CANAL	candida alb
1110	72.5	6.1	156	2	Q81516_9HEPC	hepatitis c
1111	72.5	6.1	156	2	Q81519_9HEPC	hepatitis c
1112	72.5	6.1	167	1	Q5KIU4_CRYNE	cryptococcu
1113	72.5	6.1	173	1	Q9WD17_EAV	equine arte
1114	72.5	6.1	174	2	P97065_9ENTR	salmonella
1115	72.5	6.1	180	2	P71252_ECOLI	escherichia
1116	72.5	6.1	180	2	P71254_ECOLI	escherichia
1117	72.5	6.1	180	2	P71255_ECOLI	escherichia
1118	72.5	6.1	180	2	P71256_ECOLI	escherichia
1119	72.5	6.1	180	2	P71258_ECOLI	escherichia
1120	72.5	6.1	180	2	P71259_ECOLI	escherichia
1121	72.5	6.1	180	2	P71260_ECOLI	escherichia
1122	72.5	6.1	180	2	P71261_ECOLI	escherichia
1123	72.5	6.1	183	2	Q5STJ2_CRYNE	cryptococcu
1124	72.5	6.1	191	2	Q8U4P0_PYRFU	pyrococcus
1125	72.5	6.1	208	2	O63447_ECHDI	echinotrix
1126	72.5	6.1	208	2	Q7U7L2_ECHDI	echinotrix

No.			Len	n	Accession	Description
1127	72.5	6.1	209	2	Q7JJL0_ECHDI	q7jjl0 echinotrix
1128	72.5	6.1	209	2	Q8GZ10_ARATH	q8gz10 arabidopsis
1129	72.5	6.1	209	2	Q49834_MYCLE	q49834 mycobacteri
1130	72.5	6.1	210	2	Q7JJ19_ECHDI	q7jj19 echinotrix
1131	72.5	6.1	211	2	Q7JJ13_ECHDI	q7jj13 echinotrix
1132	72.5	6.1	214	2	Q63950_ECHDI	q63950 echinotrix
1133	72.5	6.1	217	2	Q9XMK7_OCHPR	q9xmk7 ochotona pr
1134	72.5	6.1	224	2	Q8RGE6_FUSNN	q8rge6 fusobacteri
1135	72.5	6.1	243	2	Q4MHS9_BACCE	q4mhs9 bacillus ce
1136	72.5	6.1	255	2	Q7M2C0_LEIAM	q7m2c0 leishmania
1137	72.5	6.1	267	2	Q4S673_TETNG	q4s673 tetraodon n
1138	72.5	6.1	269	2	Q8RES9_FUSNN	q8res9 fusobacteri
1139	72.5	6.1	278	2	Q51160_MAGGR	q51160 magnaporthe
1140	72.5	6.1	285	2	Q86DD6_CAEEL	q86dd6 caenorhabdi
1141	72.5	6.1	291	2	O24561_MAIZE	o24561 zea mays (m
1142	72.5	6.1	298	2	Q5WL74_BACSK	q5wl74 bacillus cl
1143	72.5	6.1	298	2	Q8R2A8_MOUSE	q8r2a8 mus musculu
1144	72.5	6.1	307	2	Q6I2V8_CAEBR	q6i2v8 caenorhabdi
1145	72.5	6.1	308	2	Q6N472_RHOPA	q6n472 rhodopseudo
1146	72.5	6.1	309	2	Q71UE1_BOVIN	q71ue1 bos taurus
1147	72.5	6.1	310	2	Q5J2F7_CHIHI	q5j2f7 chimarrogal
1148	72.5	6.1	310	2	Q5WL95_BACSK	q5wl95 bacillus cl
1149	72.5	6.1	315	2	Q5WPB4_9DIPT	q5wpb4 dermatobia
1150	72.5	6.1	315	2	Q9LGO2_ARATH	q9lgo2 arabidopsis
1151	72.5	6.1	320	1	OXAA2_LACLA	oxaa2_lacla lactococcus
1152	72.5	6.1	325	2	Q9CII9_LACLA	q9cii9 lactococcus
1153	72.5	6.1	336	2	O17077_CAEEL	o17077 caenorhabdi
1154	72.5	6.1	348	2	Q83AB9_ENTFA	q83ab9 enterococcu
1155	72.5	6.1	348	2	Q99924_9TELE	q99924 cyprinella
1156	72.5	6.1	350	2	Q83SL2_ENTFA	q83sl2 enterococcu
1157	72.5	6.1	355	2	Q5UES6_ECOLI	q5ues6 escherichia
1158	72.5	6.1	356	2	Q57A42_BRUAB	q57a42 brucella ab
1159	72.5	6.1	356	2	Q8FXM4_BRUSU	q8fxm4 brucella su
1160	72.5	6.1	360	2	O70US3_DIRIM	o70us3 dirofilaria
1161	72.5	6.1	363	2	Q6HGU9_BACHK	q6hgu9 bacillus th
1162	72.5	6.1	365	2	O4L629_STAHJ	o4l629 staphylococ
1163	72.5	6.1	374	2	O8WMRO_SHEEP	o8wmro ovis aries
1164	72.5	6.1	377	2	Q4R215_VARHI	q4r215 vargula hil
1165	72.5	6.1	379	2	O8SAV3_CHIHI	o8sav3 chimarrogal
1166	72.5	6.1	379	1	Q9GBY1_OCHAL	q9gby1 ochotona al
1167	72.5	6.1	379	1	Q9GIB9_OCHCU	q9gib9 ochotona cu
1168	72.5	6.1	379	1	Q9GBY6_OCHHI	q9gby6 ochotona hi
1169	72.5	6.1	379	2	Q99GG2_OCHHY	q99gg2 ochotona hy
1170	72.5	6.1	379	2	Q9GBZ0_OCHKO	q9gbz0 ochotona ko
1171	72.5	6.1	379	1	Q9GBZ1_OCHLA	q9gbz1 ochotona la
1172	72.5	6.1	379	2	Q9GBZ2_OCHNU	q9gbz2 ochotona nu
1173	72.5	6.1	379	2	Q9GBZ3_OCHRO	q9gbz3 ochotona ro
1174	72.5	6.1	379	1	Q9GIC4_OCHRU	q9gic4 ochotona ru
1175	72.5	6.1	379	1	Q9ZZU1_OCHTH	q9zzu1 ochotona th
1176	72.5	6.1	379	1	Q9GBZ6_OCHAN	q9gbz6 ochotona an
1177	72.5	6.1	379	1	Q9GBZ7_OCHPA	q9gbz7 ochotona pa
1178	72.5	6.1	379	1	Q9GIC1_OCHHU	q9gic1 ochotona hu
1179	72.5	6.1	379	2	Q9GBY8_OCHCA	q9gby8 ochotona ca
1180	72.5	6.1	379	2	Q9GBY9_OCHCA	q9gby9 ochotona ca
1181	72.5	6.1	379	2	Q9GBY2_OCHHY	q9gby2 ochotona hy
1182	72.5	6.1	379	2	Q71LX8_OCHCA	q71lx8 ochotona ca
1183	72.5	6.1	379	2	O70UT5_OCHPR	o70ut5 ochotona pr
1184	72.5	6.1	379	2	Q9G1C3_9LAGO	q9g1c3 ochotona ca
1185	72.5	6.1	379	2	Q8EWI6_MYCPE	q8ewi6 mycoplasma
1186	72.5	6.1	379	2	Q9GAW7_9RODE	q9gaw7 chaetodipus
1187	72.5	6.1	379	2	Q508P2_9RODE	q508p2 microdipodo
1188	72.5	6.1	379	2	Q508P1_MICMC	q508p1 microdipodo
1189	72.5	6.1	379	2	Q508J6_PERPA	q508j6 perognathus
1190	72.5	6.1	379	2	Q508J4_9RODE	q508j4 perognathus
1191	72.5	6.1	387	1	P30559_9GAMA	p30559 human herpe
1192	72.5	6.1	389	1	OXYR_HUMAN	oxyr_human homo sapien
1193	72.5	6.1	402	2	O8WMQ9_SHEEP	o8wmq9 ovis aries
1194	72.5	6.1	428	2	O8ZG86_YERPS	o8zg86 yersinia pe
1195	72.5	6.1	428	2	Q66CF9_YERPS	q66cf9 yersinia ps
1196	72.5	6.1	442	2	Q6LOY3_PICTO	q6loy3 picrophilus
1197	72.5	6.1	442	2	Q6PHK5_BRARE	q6phk5 brachydanio
1198	72.5	6.1	445	2	Q6NYH8_BRARE	q6nyh8 brachydanio
1199	72.5	6.1	452	2	Q9T9N6_9BILA	q9t9n6 terebratuli

No.			Len	n	Accession	Description
1200	72.5	6.1	457	2	Q6P822_XENTR	q6p822 xenopus tro
1201	72.5	6.1	478	2	Q97OD2_SULTO	q97od2 sulfolobus
1202	72.5	6.1	488	2	Q4HEC1_CAMCO	q4hec1 campylobact
1203	72.5	6.1	488	2	Q4HLM0_CAMLA	q4hlm0 campylobact
1204	72.5	6.1	491	2	Q6SWL8_HCMV	q6swl8 human cytom
1205	72.5	6.1	499	1	MVIN_AQUAE	mvin_aquae aquifex aeo
1206	72.5	6.1	505	2	Q67658_HCMV	q67658 human cytom
1207	72.5	6.1	513	2	Q8QRY6_9BETA	q8qry6 pongine her
1208	72.5	6.1	521	1	PACR_BOVIN	pacr_bovin bos taurus
1209	72.5	6.1	522	2	Q29627_9BETA	q29627 bos taurus
1210	72.5	6.1	526	2	Q4QLL3_HAEI8	q4qll3 haemophilus
1211	72.5	6.1	528	2	O23444_CAEEL	o23444 caenorhabdi
1212	72.5	6.1	539	2	Q6FDF6_ACIAD	q6fdf6 acinetobact
1213	72.5	6.1	539	2	Q4RQI2_TETNG	q4rqi2 tetraodon n
1214	72.5	6.1	539	2	Q7VSL1_CRYPV	q7vsl1 cryptospori
1215	72.5	6.1	539	2	Q7WFK3_BORBR	q7wfk3 bordetella
1216	72.5	6.1	567	2	Q7W446_BORPA	q7w446 bordetella
1217	72.5	6.1	567	2	Q4YTZ9_PLABE	q4ytz9 plasmodium
1218	72.5	6.1	574	2	Q5F1M1_MYTGA	q5f1m1 mytilus gal
1219	72.5	6.1	614	2	Q6LH28_PHOPR	q6lh28 photobacter
1220	72.5	6.1	635	2	Q7U5J3_SYNPX	q7u5j3 synechococc
1221	72.5	6.1	642	2	Q21335_CAEEL	q21335 caenorhabdi
1222	72.5	6.1	660	2	Q8AW53_BRARE	q8aw53 brachydanio
1223	72.5	6.1	661	2	Q8AW53_BRARE	q8aw53 brachydanio
1224	72.5	6.1	662	2	Q6G493_BARHE	q6g493 bartonella
1225	72.5	6.1	662	2	Q6G146_BARQU	q6g146 bartonella
1226	72.5	6.1	666	1	KUP_STRA3	kup_stra3 streptococc
1227	72.5	6.1	670	2	Q5TYU4_BRARE	q5tyu4 brachydanio
1228	72.5	6.1	671	2	Q4IN97_GIBZE	q4in97 gibberella
1229	72.5	6.1	688	2	Q6MCRO_PARUW	q6mcro parachlamyd
1230	72.5	6.1	696	2	Q8EKS6_SHEON	q8eks6 shewanella
1231	72.5	6.1	704	2	Q8VZH3_ARATH	q8vzh3 corynebacte
1232	72.5	6.1	717	2	Q7RICO_PLAYO	q7rico plasmodium
1233	72.5	6.1	718	2	Q74IE5_LACJO	q74ie5 lactobacill
1234	72.5	6.1	718	2	Q48872_LACGK	q48872 lactobacill
1235	72.5	6.1	733	2	Q5EK43_CORJK	q5ek43 corynebacte
1236	72.5	6.1	734	2	Q9N3Y9_CAEEL	q9n3y9 caenorhabdi
1237	72.5	6.1	756	2	Q5IWR2_9POAL	q5iwr2 synechococc
1238	72.5	6.1	769	2	Q5IWR2_9POAL	q5iwr2 piptatherum
1239	72.5	6.1	803	2	Q9TU72_MUSVI	q9tu72 mustela vis
1240	72.5	6.1	832	2	Q9SIU2_ARATH	q9siu2 arabidopsis
1241	72.5	6.1	832	2	Q8VZH3_ARATH	q8vzh3 arabidopsis
1242	72.5	6.1	848	2	Q64MT1_BACFR	q64mt1 plasmodium
1243	72.5	6.1	848	2	Q5L7L5_BACFN	q5l7l5 lactobacill
1244	72.5	6.1	858	2	Q4L8R5_STAHJ	q4l8r5 lactobacill
1245	72.5	6.1	978	2	Q4UH31_THEAN	q4uh31 theileria a
1246	72.5	6.1	1103	2	Q753M8_ASHGO	q753m8 ashbya goss
1247	72.5	6.1	1238	2	Q5CUC4_CRYPV	q5cuc4 cryptospori
1248	72.5	6.1	1291	2	Q7Q409_ANOGA	q7q409 anopheles g
1249	72.5	6.1	1304	2	Q51C25_ENTHI	q51c25 entamoeba h
1250	72.5	6.1	1340	2	Q8MNJO_DICDI	q8mnjo caenorhabdi
1251	72.5	6.1	1357	2	Q55BC8_DICDI	q55bc8 dictyosteli
1252	72.5	6.1	1461	2	Q19611_CAEEL	q19611 caenorhabdi
1253	72.5	6.1	1472	2	Q4WWW3_ASPFU	q4www3 aspergillus
1254	72.5	6.1	1526	2	Q95QK2_CAEEL	q95qk2 caenorhabdi
1255	72.5	6.1	1689	2	Q8QZF4_9VIRU	q8qzf4 crimean-con
1256	72.5	6.1	1689	2	Q991H9_9VIRU	q991h9 crimean-con
1257	72.5	6.1	1702	2	Q95QK2_CAEEL	q95qk2 caenorhabdi
1258	72.5	6.1	2650	2	Q51LR8_MAGGR	q51lr8 magnaporthe
1259	72.5	6.1	4097	2	Q7RG07_PLAYO	q7rg07 plasmodium
1260	72	6.0	114	2	Q81S40_9HEPC	q81s40 hepatitis c
1261	72	6.0	156	2	Q6VRK9_HELPY	q6vrk9 equine arte
1262	72	6.0	173	2	Q5VHX9_EAV	q5vhx9 equine arte
1263	72	6.0	173	2	Q9WD22_EAV	q9wd22 equine arte
1264	72	6.0	173	2	Q9WD25_EAV	q9wd25 equine arte
1265	72	6.0	182	2	Q98815_RHILO	q98815 rhizobium 1
1266	72	6.0	185	2	Q4G3Z8_MACMU	q4g3z8 macaca mula
1267	72	6.0	200	2	Q91199_PRRSV	q91199 porcine rep
1268	72	6.0	200	2	Q91199_PRRSV	q91199 porcine rep
1269	72	6.0	209	2	Q97JJ6_CIOIN	q97jj6 ciona intes
1270	72	6.0	225	2	Q85UI0_CIOSA	q85ui0 ciona savig
1271	72	6.0	225	2	Q64FZ0_9CORO	q64fz0 avian infec
1272	72	6.0	226	2	Q6DTU8_9CORO	q6dtu8 avian infec
1273				2	Q7TEH2_9CORO	q7teh2 avian infec

Seq	S	n	E	Len	n2	Accession	Organism
1273	72	2	6.0	227	2	Q7Y6X7_TIGCA	tigriopus c
1274	72	2	6.0	239	2	O20551_URSAM	ursus ameri
1275	72	2	6.0	249	2	Q8E9R2_SHEON	shewanella
1276	72	2	6.0	254	2	Q81ZU8_BACAN	bacillus an
1277	72	2	6.0	254	2	Q81MK0_BACCR	bacillus ce
1278	72	2	6.0	266	2	Q55B22_DICDI	dictyosteli
1279	72	2	6.0	276	2	Q9HJY7_THEAC	thermoplasm
1280	72	2	6.0	279	2	Q9XXI1_CAEEL	caenorhabdi
1281	72	2	6.0	279	2	Q6HK77_BACHK	bacillus th
1282	72	2	6.0	286	2	Q6SHA6_9BACT	uncultured
1283	72	2	6.0	290	2	Q4NM76_9RICC	arthrobacte
1284	72	2	6.0	299	2	Q64R22_BACFR	bacteroides
1285	72	2	6.0	303	2	Q6HWV3_BACAN	bacillus an
1286	72	2	6.0	306	2	Q8Y980_LISMO	listeria mo
1287	72	2	6.0	306	2	Q6QDA2_LEPOC	lepisosteus
1288	72	2	6.0	311	2	Q61GS6_CAEBR	caenorhabdi
1289	72	2	6.0	311	2	Q8VF62_MOUSE	mus musculu
1290	72	2	6.0	315	2	Q5HSN1_CAMJR	campylobact
1291	72	2	6.0	317	2	Q9CK16_PASMU	pasteurella
1292	72	2	6.0	320	2	Q7ZUC3_BRARE	brachydanio
1293	72	2	6.0	323	2	Q88TJ9_LACPL	lactobacill
1294	72	2	6.0	334	2	Q88XL9_LACPL	lactobacill
1295	72	2	6.0	335	2	Q9ZY32_ORYAF	oryctolagus
1296	72	2	6.0	338	2	Q9XTR2_CAEEL	caenorhabdi
1297	72	2	6.0	339	2	Q97GD6_CLOAB	clostridium
1298	72	2	6.0	343	2	Q9B4H5_UMASC	uma scopari
1299	72	2	6.0	343	2	Q85AT6_UMASC	uma scopari
1300	72	2	6.0	343	2	Q4VTY7_SHIBO	shigella bo
1301	72	2	6.0	354	2	Q52R87_LEPOC	lepisosteus
1302	72	2	6.0	356	2	Q61CY6_CAEBR	caenorhabdi
1303	72	2	6.0	363	2	Q4VTY7_SHIBO	shigella bo
1304	72	2	6.0	364	2	Q7YWS5_CAEEL	caenorhabdi
1305	72	2	6.0	368	2	Q4KW24_9GOBI	kribia nana
1306	72	2	6.0	379	1	CYB_GEOPI	geomys pine
1307	72	2	6.0	379	1	CYB_THOMA	thomomys ma
1308	72	2	6.0	379	2	Q9THD6_ORYAF	oryctolagus
1309	72	2	6.0	379	2	Q4VWH4_TUPGL	tupaia glis
1310	72	2	6.0	379	2	Q8WDV3_CRAGY	cratogeomys
1311	72	2	6.0	379	2	Q8W8K4_CRAGY	cratogeomys
1312	72	2	6.0	379	2	Q7IIQ9_CRATY	cratogeomys
1313	72	2	6.0	379	2	Q699Q3_CRAFU	cratogeomys
1314	72	2	6.0	379	2	Q5YJ77_9RODE	geomys pers
1315	72	2	6.0	379	2	Q5YJ76_9RODE	geomys pers
1316	72	2	6.0	379	2	Q5YJ69_9RODE	geomys pers
1317	72	2	6.0	379	2	Q5YJ66_9RODE	geomys pine
1318	72	2	6.0	379	2	Q63B48_9RODE	geomys pine
1319	72	2	6.0	386	1	CYB_SARGL	sarcophyton
1320	72	2	6.0	391	2	Q8RLY7_SALET	salmonella
1321	72	2	6.0	391	2	Q8RLY9_SALET	salmonella
1322	72	2	6.0	392	2	Q9LCN9_MICEC	micromonosp
1323	72	2	6.0	396	1	CYB_LAMFL	lampetra fl
1324	72	2	6.0	396	2	Q4LW03_9BURK	burkholderi
1325	72	2	6.0	415	1	L52_ADE05	human adeno
1326	72	2	6.0	415	1	L52_ADE02	human adeno
1327	72	2	6.0	415	2	O6VGV2_9ADEN	human adeno
1328	72	2	6.0	415	2	Q71BX5_ADE01	human adeno
1329	72	2	6.0	417	2	Q9NT19_HUMAN	homo sapien
1330	72	2	6.0	418	2	Q6QFB5_LEGPN	legionella
1331	72	2	6.0	418	2	Q6QFC3_LEGPN	legionella
1332	72	2	6.0	419	2	Q66IJ4_XENTR	xenopus tro
1333	72	2	6.0	444	2	Q5HJX5_STAAC	staphylococ
1334	72	2	6.0	444	2	Q6GKS5_STAAR	staphylococ
1335	72	2	6.0	448	1	INVX_SCHPO	schizosacch
1336	72	2	6.0	448	2	Q42878_DROME	drosophila
1337	72	2	6.0	453	2	Q46034_DROME	drosophila
1338	72	2	6.0	453	2	Q7NWT7_CHRVO	chromobacte
1339	72	2	6.0	453	2	Q7A8D9_STAAM	staphylococ
1340	72	2	6.0	456	2	Q99XF2_STAAM	staphylococ
1341	72	2	6.0	462	2	Q59NM0_CANAL	candida alb
1342	72	2	6.0	464	2	Q4K0H6_STRPN	streptococc
1343	72	2	6.0	465	2	Q61H10_CAEBR	caenorhabdi
1344	72	2	6.0	467	2	Q9RDT2_STAAU	staphylococ
1345	72	2	6.0	467	2	Q57V83_9TRYP	trypanosoma
1346	72	2	6.0	468	2	Q94K50_ARATH	arabidopsis
1347	72	1	6.0	479	2	COQ6_YEAST	saccharomyc
1348	72	2	6.0	497	2	Q9FVS9_ARATH	arabidopsis
1349	72	2	6.0	514	2	Q5TYS1_ANOGA	anopheles g
1350	72	2	6.0	518	2	Q7VQX6_CANBF	candidatus
1351	72	2	6.0	523	2	Q86YB4_HUMAN	homo sapien
1352	72	2	6.0	530	2	Q65I24_ASF	african swi
1353	72	2	6.0	548	2	Q5CIG1_CRYHO	cryptospori
1354	72	2	6.0	552	2	Q6NHU7_CORDI	corynebacte
1355	72	2	6.0	553	2	Q97SL9_SULTO	sulfolobus
1356	72	2	6.0	556	2	Q55NQ9_CRYNE	cryptococcu
1357	72	2	6.0	562	2	Q93YN6_ARATH	arabidopsis
1358	72	2	6.0	584	2	Q6CF79_YARLI	yarrowia li
1359	72	2	6.0	594	2	Q7L8K9_HUMAN	homo sapien
1360	72	2	6.0	599	2	Q8R7C9_THETN	thermoanaer
1361	72	2	6.0	599	2	Q55UJ0_CRYNE	cryptococcu
1362	72	2	6.0	600	2	Q42972_SCHPO	schizosacch
1363	72	2	6.0	601	2	Q5KHV7_CRYNE	cryptococcu
1364	72	2	6.0	610	2	Q84ZX2_9CHLO	uncultured
1365	72	2	6.0	615	2	Q542R7_DICDI	dictyosteli
1366	72	2	6.0	619	2	Q4WVT3_ASPFU	aspergillus
1367	72	2	6.0	630	2	Q24608_DIACA	dianthus ca
1368	72	2	6.0	643	2	Q56SZ5_9BACT	uncultured
1369	72	2	6.0	673	2	Q61DB7_CAEBR	caenorhabdi
1370	72	2	6.0	692	2	Q6DD44_XENLA	xenopus lae
1371	72	2	6.0	692	2	Q95719_HUMAN	homo sapien
1372	72	2	6.0	696	2	Q9UBH6_HUMAN	homo sapien
1373	72	2	6.0	696	2	Q94EK6_PISUM	pisum sativ
1374	72	2	6.0	712	2	Q7N732_PHOLL	photorhabdu
1375	72	2	6.0	716	2	Q671A6_SYMTH	symbiobacte
1376	72	2	6.0	721	2	Q9VSK2_DROME	drosophila
1377	72	2	6.0	736	2	Q4HT81_CAMUP	campylobact
1378	72	2	6.0	768	2	Q660EI_BORGA	borrelia ga
1379	72	2	6.0	772	2	Q5BJ40_XENLA	xenopus lae
1380	72	2	6.0	788	2	Q50VM5_ENTHI	entamoeba h
1381	72	2	6.0	796	2	Q50VM5_ENTHI	entamoeba h
1382	72	2	6.0	844	2	Q4Q398_LEIMA	leishmania
1383	72	2	6.0	878	2	O75W8_SACCA	saccharomyc
1384	72	2	6.0	917	2	Q24809_ENTHI	entamoeba h
1385	72	1	6.0	928	2	YKD3_YEAST	saccharomyc
1386	72	2	6.0	946	2	Q4QDH8_LEIMA	leishmania
1387	72	2	6.0	980	2	P36097_PLAFK	plasmodium
1388	72	2	6.0	1025	2	Q9XXK4_CAEEL	caenorhabdi
1389	72	2	6.0	1025	2	Q7KQI4_PLAF7	plasmodium
1390	72	2	6.0	1038	1	Q98864_BRARE	brachydanio
1391	72	2	6.0	1094	2	P19334_DROME	drosophila
1392	72	2	6.0	1094	2	Q9VAE1_DROME	drosophila
1393	72	2	6.0	1113	2	Q24809_ENTHI	entamoeba h
1394	72	2	6.0	1129	2	Q4WE99_ASPFU	aspergillus
1395	72	2	6.0	1220	1	Q9C2S0_NEUCR	neurospora
1396	72	2	6.0	1275	2	Q5UQN8_MIMIV	mimivirus.
1397	72	2	6.0	1275	2	Q8EYE1_LEPIN	leptospira
1398	72	2	6.0	1282	2	Q7RVU0_NEUCR	neurospora
1399	72	2	6.0	1469	2	Q4N1M9_THEPA	theileria p
1400	72	2	6.0	1477	2	Q42597_PLABE	plasmodium
1401	72	2	6.0	1481	2	Q5CYF5_CRYPV	cryptospori
1402	72	2	6.0	1513	2	Q9QIX1_9HEPC	hepatitis c
1403	72	2	6.0	1566	2	Q9QIX2_9HEPC	hepatitis c
1404	72	2	6.0	2387	2	Q5JH15_PYRKO	pyrococcus
1405	72	2	6.0	3010	2	Q48242_9NEOP	dennyus som
1406	72	2	6.0	3010	2	Q86X19_HUMAN	homo sapien
1407	71.5	2	6.0	84	2	Q5UQN8_MIMIV	mimivirus.
1408	71.5	2	6.0	161	2	Q8EYE1_LEPIN	leptospira
1409	71.5	2	6.0	198	2	Q37682_TRYBO	trypanosoma
1410	71.5	2	6.0	200	2	Q8EYE1_LEPIN	leptospira
1411	71.5	2	6.0	206	1	VME1_IBVG	avian infec
1412	71.5	2	6.0	210	2	P05136_TRYBB	trypanosoma
1413	71.5	2	6.0	225	2	Q9GAT7_PLASM	plasmodium
1414	71.5	2	6.0	225	2	Q9GAT7_OCHCO	ochotona co
1415	71.5	2	6.0	227	2	Q7NB29_MYCGA	mycoplasma
1416	71.5	2	6.0	229	2	O3191_9HYME	monomorium
1417	71.5	2	6.0	235	2	Q7TWI5_MYCBO	mycobacteri
1418	71.5	2	6.0	237	2	O062S1_MYCTU	mycobacteri

Num			Len	N	ID	AC	Organism
1419	71.5	6.0	246	2	Q8YB21_BRUME	q8yb21	brucella me
1420	71.5	6.0	254	2	Q8LX09_9PHAE	q8lx09	laminaria d
1421	71.5	6.0	255	2	Q66480_EAV	q66480	equine arte
1422	71.5	6.0	257	2	Q71W44_LISMF	q71w44	listeria mo
1423	71.5	6.0	266	2	Q8XP47_CLOPE	q8xp47	clostridium
1424	71.5	6.0	266	2	Q5IPF5_PERAP	q5ipf5	perognathus
1425	71.5	6.0	266	2	Q5IPF3_PERPA	q5ipf3	perognathus
1426	71.5	6.0	270	2	Q8HIY5_PERLO	q8hiy5	perognathus
1427	71.5	6.0	301	2	Q9CJ24_LACLA	q9cj24	lactococcus
1428	71.5	6.0	314	1	OR39_MOUSE	or39	mus musculu
1429	71.5	6.0	320	2	Q9FAT0_VIBPA	q9fat0	vibrio para
1430	71.5	6.0	326	2	Q7L853_HUMAN	q7l853	homo sapien
1431	71.5	6.0	326	2	Q9BF45_CERSI	q9bf45	ceratotheri
1432	71.5	6.0	328	2	Q9BF57_HYLCO	q9bf57	hylobates c
1433	71.5	6.0	332	2	Q9TZ00_CAEEL	q9tz00	caenorhabdi
1434	71.5	6.0	334	2	Q9THE4_SORRA	q9the4	sorex radde
1435	71.5	6.0	336	2	O79425_NEOFO	o79425	neomys fodi
1436	71.5	6.0	336	2	O80E8_TETNG	o80e8	tetraodon n
1437	71.5	6.0	336	2	O80G2_TETNG	o80g2	tetraodon n
1438	71.5	6.0	338	2	Q4UMM1_RICFE	q4umm1	rickettsia
1439	71.5	6.0	339	2	Q8RD25_THETN	q8rd25	thermoanaer
1440	71.5	6.0	341	2	Q98RZ1_GUITH	q98rz1	guillardia
1441	71.5	6.0	341	2	Q5ND81_YERAL	q5nd81	yersinia al
1442	71.5	6.0	342	1	VG74_HHV8	vg74	human herpe
1443	71.5	6.0	342	2	O90387_HHV8	o90387	human herpe
1444	71.5	6.0	342	2	O90387_HHV8	o90387	human herpe
1445	71.5	6.0	348	1	Q77Q35_HHV8	q77q35	human herpe
1446	71.5	6.0	348	1	RNFD_VTBCH	rnfd	vibrio chol
1447	71.5	6.0	350	2	O99922_9TELE	o99922	cyprinella
1448	71.5	6.0	355	2	Q5QWM0_IDILO	q5qwm0	idiomarina
1449	71.5	6.0	360	2	Q8YDX2_BRUME	q8ydx2	brucella me
1450	71.5	6.0	362	2	Q8HIB6_9SCIU	q8hib6	callosciuru
1451	71.5	6.0	362	2	Q5CY4_BACLD	q5cy4	bacillus li
1452	71.5	6.0	366	2	Q6PDF2_MOUSE	q6pdf2	mus musculu
1453	71.5	6.0	369	2	MTR1A_SHEEP	p48040	ovis aries
1454	71.5	6.0	375	2	Q70VF8_SORMI	q70vf8	sorex minut
1455	71.5	6.0	377	2	Q6RKP7_9GAMA	q6rkp7	human herpe
1456	71.5	6.0	377	1	Q4R2I5_VARHI	q4r2i5	varcula hil
1457	71.5	6.0	379	1	Q5J15_OCHCO	q5j15	ochotona co
1458	71.5	6.0	379	1	CYB_OCHCO	cyb	ochotona fo
1459	71.5	6.0	379	1	CYB_SORRA	cyb	sorex radde
1460	71.5	6.0	379	1	CYB_SPEPA	cyb	spermophilu
1461	71.5	6.0	379	1	CYB_SPEPA	cyb	spermophilu
1462	71.5	6.0	379	2	O48007_PERAP	o48007	perognathus
1463	71.5	6.0	379	2	O8WEK3_THOTA	o8wek3	thomomys ta
1464	71.5	6.0	379	2	Q52R3_GLASA	q52r3	glaucomys s
1465	71.5	6.0	379	2	Q9TF66_SPESP	q9tf66	glaucomys s
1466	71.5	6.0	379	2	Q34661_GLASA	q34661	glaucomys s
1467	71.5	6.0	379	2	Q7IBW1_GLASA	q7ibw1	glaucomys s
1468	71.5	6.0	379	2	Q69BQ0_CRAFU	q69bq0	cratogeomys
1469	71.5	6.0	379	2	O9RODE	o9rode	liomys pict
1470	71.5	6.0	379	2	Q50BM2_9RODE	q50bm2	dipodomys d
1471	71.5	6.0	379	2	Q50BK6_9RODE	q50bk6	chaetodipus
1472	71.5	6.0	381	2	Q82ZP7_PYRAE	q82zp7	pyrobaculum
1473	71.5	6.0	381	2	Q6RKP4_9GAMA	q6rkp4	human herpe
1474	71.5	6.0	381	2	O79571_9CHON	o79571	mustelus ma
1475	71.5	6.0	382	2	Q9NYN8_HUMAN	q9nyn8	homo sapien
1476	71.5	6.0	383	1	YIY4_SCHPO	yiy4	schizosacch
1477	71.5	6.0	386	1	OXYR_PIG	oxyr	sus scrofa
1478	71.5	6.0	386	2	P32306	p32306	thermoanaer
1479	71.5	6.0	388	2	O8RB76_THETN	o8rb76	thermoanaer
1480	71.5	6.0	388	2	Q8SQ91_NYCTH	q8sq91	nycteris th
1481	71.5	6.0	390	1	Q8SQ93_9CHIR	q8sq93	nycteris gr
1482	71.5	6.0	392	2	ITR_CATCO	itr	catostomus
1483	71.5	6.0	396	2	Q9AH88_STRPN	q9ah88	streptococc
1484	71.5	6.0	404	2	Q5NIP0_PRATT	q5nip0	pratt...
1485	71.5	6.0	407	2	Q4UNI6_RICFE	q4uni6	rickettsia
1486	71.5	6.0	410	2	Q6DG01_BRARE	q6dg01	brachydanio
1487	71.5	6.0	418	2	Q82AH6_STRAW	q82ah6	streptomyce
1488	71.5	6.0	419	2	Q7NKE2_GLOVI	q7nke2	gloeobacter
1489	71.5	6.0	424	2	Q7V4C4_PROMM	q7v4c4	prochloroco
1490	71.5	6.0	424	2	Q4K127_STRPN	q4k127	streptococc
1491	71.5	6.0	431	2	Q66H32_RAT	q66h32	rattus norv
1492	71.5	6.0	435	2	Q71XN9_LISMF	q71xn9	listeria mo
1493	71.5	6.0	435	2	Q89I17_BRAJA	q89i17	bradyrhizob
1494	71.5	6.0	435	2	Q8Y5E0_LISMO	q8y5e0	listeria mo
1495	71.5	6.0	435	2	Q8Y5E0_LISIN	q8y5e0	listeria in
1496	71.5	6.0	444	2	Q929P5_LISIN	q929p5	listeria in
1497	71.5	6.0	453	2	Q62527_CAEBR	q62527	caenorhabdi
1498	71.5	6.0	453	2	Q55L80_CRYNE	q55l80	cryptococcu
1499	71.5	6.0	453	2	Q5KAA2_CRYNE	q5kaa2	cryptococcu
1500	71.5	6.0	464	2	Q59Q41_CANAL	q59q41	candida alb
		6.0	464	2	Q59Q41_CANAL	q59q41	candida alb
		6.0	466	2	Q5AZ68_EMENI	q5az68	aspergillus

ALIGNMENTS

RESULT 1

MENTO_HUMAN

ID   MENTO_HUMAN   STANDARD;   PRT;   234 AA.
AC   O95772;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   MLN64 N-terminal domain homolog (START3 N-terminal-like protein).
GN   Name=STARD3NL; Synonyms=MENTO; ORFNames=UNQ955/PRO1864;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;

RN   [1]
RP   NUCLEOTIDE SEQUENCE, CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND
RP   ALTERNATIVE INITIATION.
RC   TISSUE=Fetal brain;
RX   MEDLINE=22384343; PubMed=12393907; DOI=10.1074/jbc.M208290200;
RA   Alpy F., Wendling C., Rio M.-C., Tomasetto C.;
RT   "MENTO, a MLN64 homologue devoid of the START domain.";
RL   J. Biol. Chem. 277:50780-50787(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow T.W., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Arnett C., Wohldmann P., Le T.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain, and Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
RA   Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.,
RA   Schein J.E.; Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC   membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative initiation;
CC   Comment=2 isoforms, 1 (shown here) and 2, are produced by
CC   alternative initiation;
CC   -!- PTM: Phosphorylated.
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!-
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -!-
DR   EMBL; AJ492267; CAD37353.1; -; mRNA.
DR   EMBL; AY358645; AAQ89008.1; -; mRNA.
DR   EMBL; AC006033; AAS07552.1; -; Genomic_DNA.
DR   EMBL; AC003074; -; -; Genomic_DNA.
DR   EMBL; BC005959; AAH03074.1; -; mRNA.
DR   EMBL; BC005959; AAH05959.1; -; mRNA.
DR   Ensembl; ENSG00000010270; Homo sapiens.
DR   HGNC; HGNC:19169; STARD3NL.
KW   Alternative initiation; Phosphorylation; Transmembrane.
FT   CHAIN   1   234   MLN64 N-terminal domain homolog, isoform
FT   1.
FT   CHAIN   8   234   MLN64 N-terminal domain homolog, isoform
FT   2.
FT   INIT_MET   8   8   For isoform 2.
FT   TOPO_DOM   1   53   Cytoplasmic (Potential).
FT   TRANSMEM   54   74   Potential.
FT   TOPO_DOM   75   97   Extracellular (Potential).
FT   TRANSMEM   98   118   Potential.
FT   TOPO_DOM   119   122   Cytoplasmic (Potential).
FT   TRANSMEM   123   143   Potential.
FT   TOPO_DOM   144   150   Extracellular (Potential).
FT   TRANSMEM   151   171   Potential.
FT   TOPO_DOM   172   234   Cytoplasmic (Potential).
FT   DOMAIN   48   218   MENTAL.
SQ   SEQUENCE   234 AA; 26655 MW; AFB7DAE381983FB0 CRC64;

Query Match   100.0%; Score 1195; DB 1; Length 234;
Best Local Similarity   100.0%;
Matches 234; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60

Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRL 120

Qy   121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180

Qy   181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL 234
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL 234

RESULT 2
ID   Q5U205_RAT   PRELIMINARY;   PRT;   235 AA.
AC   Q5U205;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
.

DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   STARD3 N-terminal like (Predicted).
GN   Name=Stard3nl_predicted;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RC   DIRECTOR MGC Project;
RA   Strausberg R.L.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC086352; AAH86352.1; -; mRNA.
SQ   SEQUENCE   235 AA; 26718 MW; 6238B671397EA775 CRC64;

Query Match   95.5%; Score 1141.5; DB 2; Length 235;
Best Local Similarity   95.7%;
Matches 225; Conservative   3; Mismatches   6; Indels   1; Gaps   1;

Qy   1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
              ||||||||||.|||||||||||.||||||..||||||||||||||||||||||||||||||
Db   1 MNHLPEDMENTLTGSQSSHASLRDIHSINPGGQLMARIESYEGREKKGISDVRRTFCLFVT 60

Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRL 120
              |||||||||||||||||||||||.|||.|.|||||||||||||||||||||.||.||||||
Db   61 FDLLFVTLLWIIELNVNGGIENTLKKEVAHDYSSYFDIFLLAVFRFKVLLGYAVCRL 120

Qy   121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180

Qy   181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSEE-EEAEEKQDSEKPLLEL 234
              |||||||||||||||||||||:|||||||||||||||||| ||||||||||||||||
Db   181 EEENRLLIVQDASERAALIPAGLSDGQFYSPPESEAGSEE-EEAEEKQDSEKPLLEL 235

RESULT 3
ID   MENTO_MOUSE   STANDARD;   PRT;   235 AA.
AC   Q9DCI3; Q99J63; Q9D356;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   MLN64 N-terminal domain homolog (STARD3 N-terminal-like protein).
GN   Name=Stard3nl; Synonyms=Mento;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC   ---
CC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
CC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Kidney;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., McKenan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Fahey J., Helton E., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Whiting M., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC   membrane protein (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC   Name=1;
CC   IsoId=Q9DCI3-1; Sequence=Displayed;
CC   Name=2;
CC   IsoId=Q9DCI3-2; Sequence=VSP_003909;
CC   Note=No experimental confirmation available;
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- CAUTION: Ref.1 (BAB31166) sequence differs from that shown due to
CC   a frameshift in position 31.

KW   Alternative splicing; Transmembrane.
FT   TOPO_DOM   1   53   Cytoplasmic (Potential).
FT   TRANSMEM   54   74   Potential.
FT   TOPO_DOM   75   97   Extracellular (Potential).
FT   TRANSMEM   98   118   Potential.
FT   TOPO_DOM   119   122   Cytoplasmic (Potential).
FT   TRANSMEM   123   143   Potential.
FT   TOPO_DOM   144   150   Extracellular (Potential).
FT   TRANSMEM   151   171   Potential.
FT   TOPO_DOM   172   235   Cytoplasmic (Potential).
FT   DOMAIN   48   218   MENTAL.
FT   VARSPLIC   218   235   SEEAEEKQESEKPLLEL -> RNSSAPRMGIQKSSQPSGG
FT   AAGTRARFVPKASSCREGRPCLPMMLQ (in isoform
FT   2).
FT   CONFLICT   32   33   /FTId=VSP_003909
FT   CONFLICT   52   52   QL -> HS (in Ref. 1; BAB22337).
FT   R -> G (in Ref. 2).
SQ   SEQUENCE   235 AA; 26811 MW; F2517Z5390CB1503 CRC64;

Query Match   94.9%; Score 1134.5; DB 1; Length 235;
Best Local Similarity   94.9%; Pred. No. 2.9e-95;
Matches 223; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

Qy   1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
              ||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||
Db   1 MNHLPEHMENTLTGSQSSHASLRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLFVT 60

Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVLILAYAVCRL 120
              |||||||||||||||||||||||| |||||||:|||||||||:|||||||||||||||
Db   61 FDLLFVTLLWIIELNVNGGIENTLKKEVIHYDYSSYFDIFLLAVRFKVLILGYAVCRL 120

Qy   121 RHWWAIALITTAVTSAFLLAKVILSKLFSQGAFGYVLPIISPILAWIETWFLDFKVLPQEA 180
              |||||||:||||||||||||||||||||||| ||||||||||:|||||||||||||||||
Db   121 RHWWAIALTTAVTSAFLLAKVILSKLFSQDAFGYVLPIISPILAWIETWFLDFKVLPQEA 180

Qy   181 EEENRLLIVQDASERAALIPGGLSDGQFYdPPESEAGS--EEAEEKQDSEKPLLEL 234
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   181 EEENRLLIVQDASERAALIPAGLSDGQFYdPPESEAGSEEEAEEKQESEKPLLEL 235

RESULT 4
ID   Q6DI38_BRARE PRELIMINARY; PRT; 227 AA.
AC   Q6DI38;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   ZGC:86628.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Left column

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC075752; AAH75752.1; -; mRNA.
DR ZFIN; ZDB-GENE-040718-4; zgc:86628.
SQ SEQUENCE 227 AA; 25485 MW; 24C46AD8FF4985C6 CRC64;

Query Match 66.6%; Score 796; DB 2; Length 227;
Best Local Similarity 68.3%; Pred. No. 2.4e-64;
Matches 155; Conservative 31; Mismatches 39; Indels 2; Gaps 2;

```
Qy    8 MENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLFVT   67
          |||||:|||||||||||:|||:|||||||||||||||||||||||||||||||||||||
Db    1 MDSQCSSSVGSRANLGGLGNINSTPISARVESYEAGEKKGISDVRRTFCLFVTFDLLFVT   60

Qy   68 LLWIIELNVNGGIGENTLEKEVMQYDYYSSYFDIFLLAVRFRKVILLAYAVCRLRHWAIA  127
          |||:|:||||||||||||:||:||||||||||||||||||||||||||||||:||||
Db   61 LLWIIELNVNGGIQQOLEQEVLKYDYHKSFPDIFLLAVFRFAALILAYAVCKLRHWAIA  120

Qy  128 LTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAEEENRLL  187
          |:||:||||||:|||||||||:|||||||||||||||||||||||||||||:::|||
Db  121 ITTAITTGFLIVKVVVSKLLSQGAFGYLLPIISFILAWIETWLLDFKVLPQEAGDEJRYL  180

Qy  188 IVQDASERAALI-PGGLSDGQFYSPSPPESEAGS-EEAEEKQDSEKPLL  232
          |:|:   ||||:|||||||||||||||||| :|||::||:|||||:
Db  181 SVQNRLEHEPLLPDGPLSEGLFYSPSPESLADSDEDLDDKHDLEKPIV  227
```

RESULT 5
ID   Q6DPR7_XENTR PRELIMINARY; PRT; 448 AA.
AC   Q6DPR7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   START domain containing 3.
GN   Name=stard3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Right column

RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Green E.D., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC076666; AAH76666.1; -; mRNA.
SMR; Q6DPR7; 236-443.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0005484; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0008289; F:lipid binding; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE 448 AA; 50926 MW; 2686D07C737D4204 CRC64;

Query Match 58.6%; Score 700.5; DB 2; Length 448;
Best Local Similarity 61.1%; Pred. No. 2.8e-55;
Matches 143; Conservative 29; Mismatches 49; Indels 13; Gaps 4;

```
Qy    1 MNHLP----EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC   56
          |:||:       ||:|||||||||||||||:|||:||||||||||||||||||||||||
Db    1 MTKLPGDFQPDLERSLPAIASINSSMSQNHVFSPHSLLPR------EQRVISDVRRTFC   54

Qy   57 LFVTFDLLFVTLLWIIELNVNGGIGENTLEKEVMQYDYYSSYFDIFLLAVRFRFSVLLAYA  116
          |||||||||||||||||:||||||||||||||||:||::|||||||||||||:||||||||
Db   55 LFVTFDLLFISLLWIIELNTNDGIEKNLEEILHYDFKNSFPDIFLLAVFRFSVLLAYA  114

Qy  117 VCRLRHWWAIALITTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL  176
          |||||||||:||||||:||||||||:|||| |||::|||||||:|||||||||||||||||
Db  115 IVRLRHWWAIAITTLVTSAFLIAKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL  174

Qy  177 PQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPSPPESEAGSEAEAEEKQDSEK  229
          ||||::||:||:|||||||||||||||||||||||||||||||||::|:||:  :||
Db  175 TQEAEEERWYMAVQAAGSHPPLIYNGALSDGQFYSPSPPESFAGSD-NEFDDDEE  226
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RESULT 6
ID   Q6PF40_XENLA PRELIMINARY; PRT; 444 AA.
AC   Q6PF40;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

DE   MGC68989 protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Q6PF40; 232-439.
SMR; Q6PF40; 232-439.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR GO; GO:0006694; P:steroid biosynthesis; IEA.
DR InterPro; IPR000799; StAR.
DR InterPro; IPR002913; START.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS50848; START; 1.
SQ SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;

Query Match   58.5%; Score 698.5; DB 2; Length 444;
Best Local Similarity 60.9%; Pred. No. 4.2e-55;
Matches 140; Conservative 30; Mismatches 51; Indels 9; Gaps 3;

Qy   1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
         ||||| |:||| |||||:|:| || |::| :|:: |:| || :::
Db   1 MTKIPGDFQPDLERSLPAIASMSQSHVFSPRSLLPR-----EQRRAISDVRRTFCLFVT 54

Qy   61 FDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVRFRKVLILAYAVCRL 120
         ||||:|||||||| :|||||||||| :|| ||:||::::|::||||||| || |:|::|:
Db   55 FDLLFISLLWIIELNTNNGIEKNLEEILIYDFKNSFFDIFLLAVRFSVLILAYAIVRL 114

Qy 121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGARGYVLPIISFTLAWIETWFLDFKVLPQEA 180
         ||||:||| |||||:|||: |::| |||| :||||||:||||||||||| |||||| |||
Db 115 RHWWAIAITLVTSAFLIVKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVLTQEA 174

Qy 181 EEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEEAEEKQDSEK 229
         ||| :|:|:| ||:||:|:||:|||| ||||||||| || ||:|||
Db 175 EEERWIIAAQAAATHPSLLYNGALSDGQFYSPPESPAGSD--NEFDDEEE 222

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MGC80895 protein.
GN Name=MGC80895;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
SMR; Q6GNT3; 236-443.
EMBL; BC073419; AAH73419.1; -; mRNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0008669; P:lipid transport; IEA.
DR GO; GO:0006694; P:steroid biosynthesis; IEA.
DR InterPro; IPR000799; StAR.
DR InterPro; IPR002913; START.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS50848; START; 1.
SQ SEQUENCE 448 AA; 51279 MW; 472F8E7C3B2F5E4 CRC64;

Query Match   57.2%; Score 684; DB 2; Length 448;
Best Local Similarity 59.7%; Pred. No. 9e-54;
Matches 139; Conservative 34; Mismatches 48; Indels 12; Gaps 4;

Qy   1 MNHLP-----EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC 56
         ||||| | | :|||| |||||:|:| || |::| :|:: |:| || :::
Db   1 MTKLPGEFQPDLERSLPAIASINSSMSHNHVPSPHSLLPR-----EQRRLISDVRRTFC 54

Qy   57 LFVTFDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVRFRKVLILAYA 116
         ||||||||:|||||||| :|||||||||| :|| ||:||::::|::||||||| || |

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Db
Qy   55 LFVTFDLLFISLLWIIEILNNTNNGIEKNLEEEILHYDFKNSFPDIYLLAVPRFSVLILAVA 114
           ||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db  117 VCRLRHWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL 176
Qy  117 IVRLRHWAIAITTLVTSAFLIVKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL 174
           | ||||||| |||||| |||| || | |||||||||||||||||| |||||||||
Db  115 IVRLRHWAIAITTLVTSAFLIVKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL 174

DE  177 PQEAEEENRLLIVQ-DASERAALLPGGLSDGQYPYPPESEAGSE-EAEEKQDS 227
           |||||||||||||  | |||||||||||||||||||| ||||:||| ::::
Qy  177 PQEAEEERWYTAAQAPANHPPYLYNGTLSDGQFYSPPESPAGSDNEFEDEEEA 227
           |||:|||||| : || | |||||:|||||||||||||| |||||:|:|:
Db  175 TQEAEEERWYTAAQAPANHPPYLYNGTLSDGQFYSPPESPAGSDNEFEDEEEA 227
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RESULT 8
ID   MLN64_HUMAN   STANDARD;   PRT;   445 AA.
AC   Q14849; Q96HM9;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   MLN 64 protein (StAR-related lipid transfer protein 3) (StARD3) (START
DE   domain-containing protein 3) (CAB1 protein).
GN   Name=STARD3; Synonyms=CAB1, MLN64;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary carcinoma;
RX   MEDLINE=96039245; PubMed=7490069;
RA   Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M-G.,
RA   Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT   "Identification of four novel human genes amplified and overexpressed
RT   in breast carcinoma and localized to the q11-q21.3 region of
RT   chromosome 17.";
RL   Genomics 28:367-376(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Oesophageal carcinoma;
RX   MEDLINE=97413641; PubMed=9270027;
RA   Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M.,
RA   Hirai H., Yazaki Y., Sugimura T., Terada M.;
RT   "Isolation of a candidate gene, CAB1, for cholesterol transport to
RT   mitochondria from the c-ERBB-2 amplicon by a modified cDNA selection
RT   method.";
RL   Cancer Res. 57:3548-3553(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung, Skin, and Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445.
RX   MEDLINE=20264523; PubMed=10802740; DOI=10.1038/75192;

RA   Tsujishita Y., Hurley J.H.;
RT   "Structure and lipid transport mechanism of a StAR-related domain.";
RL   Nat. Struct. Biol. 7:408-414(2000).
RN   [5]
RP   TOPOLOGY.
RX   MEDLINE=21264925; PubMed=11033434; DOI=10.1074/jbc.M006279200;
RA   Alpy F., Stoeckel M.-E., Dierich A., Escola J.-M., Wendling C.,
RA   Chenard M.-P., Vanier M.T., Gruenberg J., Tomasetto C., Rio M.-C.;
RT   "The steroidogenic acute regulatory protein homolog MLN64, a late
RT   endosomal cholesterol-binding protein.";
RL   J. Biol. Chem. 276:4261-4269(2001).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC   steroidogenesis in placenta and brain.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC   membrane protein.
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- SIMILARITY: Contains 1 START domain.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC   WWW="http://www.infobiogen.fr/services/chromcancer/Genes/MLN64ID202.html".
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; X80198; CAA56489.1; -; mRNA.
DR   EMBL; D38255; BAA22525.1; -; mRNA.
DR   EMBL; BC008356; AAH08356.1; -; mRNA.
DR   EMBL; BC008747; AAH08747.1; -; mRNA.
DR   EMBL; BC025679; AAH25679.1; -; mRNA.
DR   PIR; I38027; I38027.
DR   PDB; 1EM2; X-ray; A=216-444.
DR   Ensembl; ENSG00000131748; Homo sapiens.
DR   HGNC; HGNC:17579; STARD3.
DR   H-InvDB; HIX0013780; -.
DR   MIM; 607048;
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0008203; P:cholesterol metabolism; TAS.
DR   GO; GO:0006629; P:lipid metabolism; TAS.
DR   GO; GO:0006839; P:mitochondrial transport; TAS.
DR   GO; GO:0008202; P:steroid metabolism; TAS.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   3D-structure; Lipid transport; Lipid-binding; Steroidogenesis;
KW   Transmembrane; Transport.
FT   TOPO_DOM   1   51   Cytoplasmic (Potential).
FT   TRANSMEM   52   72   Potential.
FT   TOPO_DOM   73   94   Extracellular (Potential).
FT   TRANSMEM   95   115   Potential.
FT   TOPO_DOM   116   120   Cytoplasmic (Potential).
FT   TRANSMEM   121   141   Potential.
FT   TOPO_DOM   142   148   Extracellular (Potential).
FT   TRANSMEM   149   169   Potential.
FT   TOPO_DOM   170   445   Cytoplasmic (Potential).
FT   DOMAIN   46   217   MENTAL.
FT   DOMAIN   230   443   START.
FT   CONFLICT   117   117   Q -> R (in Ref. 3; AAH08356/AAH25679).
FT   CONFLICT   216   216   G -> A (in Ref. 3; AAH25679).
FT   HELIX   233   253
FT   TURN   254   255
FT   HELIX   256   258
FT   STRAND   260   264
FT   TURN   266   267
FT   STRAND   270   276
FT   TURN   277   279
FT   STRAND   280   289
FT   HELIX   293   299
FT   TURN   300   302
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FT   HELIX      304    307
FT   TURN       308    310
FT   TURN       312    313
FT   STRAND     314    323
FT   STRAND     324    326
FT   STRAND     327    334
FT   STRAND     337    337
FT   STRAND     338    341
FT   TURN       342    342
FT   TURN       345    355
FT   STRAND     359    366
FT   STRAND     379    380
FT   STRAND     382    383
FT   STRAND     386    392
FT   TURN       397    398
FT   TURN       400    406
FT   STRAND     408    409
FT   HELIX      416    440
FT   TURN       441    442
SQ   SEQUENCE   445 AA;  50474 MW;  62BED5C3EDA0DDEF CRC64;
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Query Match             55.6%;  Score 664;  DB 1;  Length 445;
Best Local Similarity   56.2%;  Pred. No. 6e-52;
Matches 135;  Conservative 38;  Mismatches 45;  Indels 22;  Gaps 5;

Qy   1    MNHLP-----EDMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV  51
          |:|:   ||||||       ||:|||||||||||||||:||||||:|||||||||||||
Db   1    MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHLLPPE---------------KRRAISDV  49
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Qy   52   RRTFCLFVTFDLLFVTLLMIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVPRFKVL  111
          |||||||||||||:|:|||||||||||||||||||||||:|||||:||||||||||||||
Db   50   RRTFCLFVTFDLLFISLLMIIELNTNTGIRKNLEQIIIQYNFKTSFPDIFVLAFPRFSGL  109
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Qy   112  ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL  171
          |||||:|||||||||:||||||||||||||||||||||||:|||||||||||||||||||
Db   110  LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL  169
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Qy   172  DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK  229
          ||||||||||||||||||||||||||||  ||:|:|||||||||||||||  ||:|:|||
Db   170  DFKVLPQEAEEERWILAAQVAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVAGKK  229
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Query Match             55.6%;  Score 664;  DB 2;  Length 445;
Best Local Similarity   56.2%;  Pred. No. 6e-52;
Matches 135;  Conservative 38;  Mismatches 45;  Indels 22;  Gaps 5;

Qy   1    MNHLP-----EDMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV  51
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RESULT 9
Q53Y53_HUMAN
ID   Q53Y53    PRELIMINARY;    PRT;    445 AA.
AC   Q53Y53;
DT   13-SEP-2005  (TrEMBLrel. 31, Created)
DT   13-SEP-2005  (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005  (TrEMBLrel. 31, Last annotation update)
DE   START domain containing 3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT006964; AAP35610.1; -; mRNA.
SQ   SEQUENCE   445 AA;  50474 MW;  62BED5C3EDA0DDEF CRC64;
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RESULT 10
MLN64_MOUSE
ID   MLN64_MOUSE    STANDARD;    PRT;    446 AA.
AC   Q61542;
DT   30-MAY-2000  (Rel. 39, Created)
DT   30-MAY-2000  (Rel. 39, Last sequence update)
DT   10-MAY-2005  (Rel. 47, Last annotation update)
DE   MLN 64 protein (StAR-related lipid transfer protein 3) (StARD3) (START
DE   domain-containing protein 3) (ES 64 protein).
GN   Name=Stard3; Synonyms=Es64, Mln64;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=96039245; PubMed=7490069;
RA   Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA   Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT   "Identification of four novel human genes amplified and overexpressed
RT   in breast carcinoma and localized to the q11-q21.3 region of
RT   chromosome 17.";
RL   Genomics 28:367-376(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis in placenta and brain (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein (By similarity).
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- SIMILARITY: Contains 1 START domain.
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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```
Qy   52   RRTFCLFVTFDLLFVTLLMIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVPRFKVL  111
          |||||||||||||:|:|||||||||||||||||||||||:|||||:||||||||||||||
Db   50   RRTFCLFVTFDLLFISLLMIIELNTNTGIRKNLEQIIIQYNFKTSFPDIFVLAFPRFSGL  109
```

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Qy   112  ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL  171
          |||||:|||||||||:||||||||||||||||||||||||:|||||||||||||||||||
Db   110  LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL  169
```

```
Qy   172  DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK  229
          ||||||||||||||||||||||||||||  ||:|:|||||||||||||||  ||:|:|||
Db   170  DFKVLPQEAEEERWILAAQVAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVAGKK  229
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Qy   1    MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHLLPPE---------------KRRAISDV  49
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CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; X82457; CAA57834.1; -; mRNA.
DR   EMBL; BC003313; AAH03313.1; -; mRNA.
DR   Ensembl; ENSMUSG00000018167; Mus musculus.
SMR; Q61542; 231-444.
HSSP; Q14849; 1EM2.
MGI; MGI:1929618; Stard3.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005770; C:late endosome; TAS.
GO; GO:0000799; C:late endosome; TAS.
InterPro; IPR000799; StAR.
GO; GO:0005770; C:integral to membrane; TAS.
Pfam; PF01852; START; 1.
PRINTS; PR00978; STARPROTEIN.
SMART; SM00234; START; 1.
PROSITE; PS50848; START; 1.
KW   Lipid transport; Lipid-binding; Steroidogenesis; Transmembrane;
KW   Transport.
FT   TOPO_DOM      1     52       Cytoplasmic (Potential).
FT   TRANSMEM     53     73       Potential.
FT   TOPO_DOM     74     95       Extracellular (Potential).
FT   TRANSMEM     96    116       Potential.
FT   TOPO_DOM    117    121       Cytoplasmic (Potential).
FT   TRANSMEM    122    142       Potential.
FT   TOPO_DOM    143    149       Extracellular (Potential).
FT   TRANSMEM    150    170       Potential.
FT   TOPO_DOM    171    446       Cytoplasmic (Potential).
FT   DOMAIN      218    446       START.
FT   DOMAIN      231    444       MENTAL.
FT   DOMAIN       47    218       Cytoplasmic (Potential).
SQ   SEQUENCE    446 AA;  50470 MW;  DBF4359604F3E1E2 CRC64;
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```
Qy          7  DMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTF   61
               :  ||        |||||||||||||||||||||||||||||||||||||||||||||||||
Db         11  DLERSLPALASLGTSLSHSQSLSSHFIPPPL------------EKRAISDVRRTFCLFVTF   60

Qy         62  DLLFVTLLMWIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLR  121
               ||::|:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61  DLLFISLLMIELNTNTGIRKNLEQEVIHYSFQSSFDIFVLAFFRFSGLLLGYAVLRLQ  120

Qy        122  HWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAE  181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121  HWWVIAVTLLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFLDFKVLPQEAE  180

Qy        182  EENRLLIVQDASERAALI-PGGLSDGQFYSPPESSAGSE-EAEEKQDSEK  229
               :::||||||||||||||| |||||||||||||||||||| :||||:||||
Db        181  EERWYLAAQAAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVTGKK  230
```

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Query Match           54.9%;  Score 656.5;  DB 1;  Length 446;
Best Local Similarity 57.8%;  Pred. No. 2.9e-51;
Matches 133;  Conservative  33;  Mismatches  47;  Indels  17;  Gaps  4;
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RESULT 11
Q5U2T5_RAT
ID   Q5U2T5_RAT             PRELIMINARY;    PRT;     446 AA.
AC   Q5U2T5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical LOC363675.
GN   Name=LOC363675;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=22382857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
```

```
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC085872; AAH85872.1; -; mRNA.
SMR; Q5U2T5; 231-444.
SQ   SEQUENCE    446 AA;  50385 MW;  19BF58B56F09722F CRC64;
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0008289; F:lipid binding; IEA.
DR   GO; GO:0008289; F:lipid binding; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   GO; GO:0006700; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Hypothetical protein.
```

```
Qy          1  MNHLPEDMEN--------ALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV   51
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Db          1  MSKLPGDLAGDLERSLPALASLGTSLSHSQSLSSHFIPPPLEKRRV------------VSDV   50

Qy         52  RRTFCLFVTFDLLFVTLLMWIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVL  111
               |||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db          1  RRTFCLFVTFDLLFISLLMIELNTNTGIRKNLEQEVIHYSFQSSFDIFVLAFFRFSGL  110

Qy        112  ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL  171
               ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db         51  LLGYAVLRLQHWWVIAITTLVSSAFLIVKVILSELLSKGARGYLLPIVSFVLAWLETWFL  170

Qy        172  DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESSAGSE-EAEEKQDSEK  229
               |||||||||||:||:|||||||||||||| ||||||||||||||||||| ::|||:||||
Db        171  DFKVLPQEAEERWYLAAQAAVARGPLLFSGALSEGQFYSPPESFAGSDSDESDEEVAGKK  230
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Query Match           54.9%;  Score 656.5;  DB 2;  Length 446;
Best Local Similarity 56.2%;  Pred. No. 2.9e-51;
Matches 135;  Conservative  32;  Mismatches  52;  Indels  21;  Gaps  4;
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```
RESULT 12
Q544C3_MOUSE
ID   Q544C3_MOUSE           PRELIMINARY;    PRT;     446 AA.
AC   Q544C3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A630020B16 product:steroidogenic acute regulatory protein
DE   related, full insert sequence.
GN   Name=Stard3;
```

OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C.A., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RC   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384 format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numata R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Suzuki H., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK041538; BAC30977.1; -; mRNA.
DR   MGI; MGI:1929618; Stard3.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005770; C:late endosome; TAS.
SQ   SEQUENCE   446 AA;   50469 MW;   DBF43S9604F3E1E2 CRC64;

Query Match   54.9%; Score 656.5; DB 2; Length 446;
Best Local Similarity 57.8%; Pred. No. 2.9e-51;
Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;

Qy   7 DMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTF 61
            |: |:| |: ::||:: : |||: || || ||: ||::| ||| ||::|
Db   11 DLERSLPALASLGTSLSHSQSLSSHPIPPL----------EKRRAISDVRRTFCLFVTF 60

Qy   62 DLLFVTLLWIIIELNVNNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVILLAYAVCRLR 121
            |||| || || |||| :|| ||| ||||| |::|||||| ||| | || || ||| |
Db   11 DLLFISLLWIIELNTNTGIRKNLEQEVIHYSFQSSFFDIFVLAFFRRSGLLLGYAVLRLQ 120

Qy   122 HWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISPILAWIETWFLDFKVLPQEAE 181
            |||| ||:|| :||| ||||| || || |: ||| : | || ||| ||||||||||||
Db   121 HWWVIAVTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFLDFKVLPQEAE 180

Qy   182 EENRLLIVQDASERAALI-PGGLSDCGFYSPPESEAGSE-EAEEKQDSEK 229
            |||| |:| |||: | || || ||| || ||||| |: ||||||||: |
Db   181 EERWYLAAQAAVARGPLLFSGALSEGQPYSPESFAGSDNESDEEVTGKK 230

RESULT 13
MLN64_BRARE

ID   MLN64_BRARE   STANDARD;   PRT;   448 AA.
AC   Q9DFS4; Q6FH03;
DT   28-FEB-2003 (Rel. 41, Created)
DT   01-FEB-2005 (Rel. 46, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   MLN64-like protein (START domain-containing protein 3).
GN   Name=stard3; Synonyms=mln64;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

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OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=AB;
RG   NIH - Zebrafish Gene Collection (ZGC) project;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 210-448.
RX   PubMed=11064158; DOI=10.1016/S0303-7207(00)00316-6;
RA   Bauer M.P., Bridgham J.T., Langenau D.M., Johnson A.L., Goetz F.W.;
RT   "Conservation of steroidogenic acute regulatory (StAR) protein
RT   structure and expression in vertebrates.";
RL   Mol. Cell. Endocrinol. 168:119-125(2000).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis (By similarity).
CC   -!- SIMILARITY: Contains 1 START domain.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; BC056766; AAH56766.1; -; mRNA.
DR   EMBL; AF258786; AAG28603.1; -; mRNA.
DR   HSSP; Q14849; 1EM2.
DR   SMR; Q9DFS4; 232-443.
DR   ZFIN; ZDB-GENE-001120-2; stard3.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Lipid transport; Lipid-binding; Steroidogenesis; Transport.
FT   DOMAIN      232    445    START
FT   CONFLICT    210    220    YSPPESLAGSE -> PGRPRVRPRVR (in Ref. 2).
SQ   SEQUENCE   448 AA;  50751 MW;  716A18C127B59C5D CRC64;
```

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Query Match             52.9%;  Score 632;  DB 1;  Length 448;
Best Local Similarity   70.9%;  Pred. No. 5.1e-49;
Matches 127;  Conservative 18;  Mismatches 32;  Indels 2;  Gaps 2;

Qy    44  EKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLL 103
              ||||||||||||||||||| ||||||||||||||| |:|| ||||||||||
Db    43  ERKAPSDVRRTFCLFVTFDLLFITLLWIIELNISKSIWNSLENEVHYNKSSFFDIFLL 102

Qy   104  AVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFIL 163
              ||||  |||||||||||||||| |||||||||||||||||||  ::|
Db   103  AVFRFLCLQLGYAAFRLRHWVIAITTLVTTAFLIAKVILSDLFSQNAFGYVLPITSFVV 162

Qy   164  AWIETWFLDFKVLPQEAEEEN-RLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEE 220
              ||||||||||||  | :||| |||:||| |||| | |||||||||||||||:||||
Db   163  AWLETWFLDFKVLTQEAEDERVLAAVNAACEPAPLICRPRPVSDGQFYSPPESLAGSED 221
```

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OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014700; CAG02839.1; -; Genomic_DNA.
NON_TER   1
NON_TER   1
SQ   SEQUENCE   444 AA;  50312 MW;  0A2E1D687EDB2C41 CRC64;
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Query Match             49.1%;  Score 586.5;  DB 2;  Length 444;
Best Local Similarity   55.2%;  Pred. No. 7.2e-45;
Matches 122;  Conservative 30;  Mismatches 42;  Indels 27;  Gaps 5;

Qy    12  LTGSQSSHASLRNIHS-----INPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLFVT 67
              :: ||:::| ::  :    ||||||||||  :||||||||||||||||||||
Db     5  ISNLNSSHSTLLSLPSPYLFVPPA------ARKTISDVRRTFCLFVTFDLLFIS 52

Qy    68  LLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIA 127
              ||||||||  ||||||||||||||||||||||||  |::||||||||||||||||
Db    53  LLWIIELNISNSLKRSLINHEVVHYDYRSSFFDIFLLAVFRFLCLQLGYAAFRLRHWVVA 112

Qy   128  LTTAVTSAFLLAKVILS----------KLFSQGAFGYVLPIISFILLAWIETWFLDFKVLPQ 178
              :||| ||||:|||  |           ||||||||||||||:||| |||||||||||
Db   113  VTTLVTCVFLVVKLILSNNNANSGSDNLLSQNAFGYVLPITSFVVAWLETWFLDFKVLTQ 172

Qy   179  EAEEENRLLIVQDAS-ERAALI-PGGLSDGQFYSPPESEAG 217
              ||:|| |||:|||| ||||| |||||||||||||||||
Db   173  EADDERAYLAAVNASCERSPMIYPRPVSDGQFYSPPESIAG 213
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RESULT 14
Q4S943 TETNG
ID   Q4S943_TETNG  PRELIMINARY;  PRT;  444 AA.
AC   Q4S943;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 3 SCAF14700, whole genome shotgun sequence.
DE   (Fragment).
OS   ORFNames=GSTENG00022066001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontoidea; Tetraodontidae; Tetraodon.
```

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RESULT 15
Q5RB70 PONPY
ID   Q5RB70_PONPY  PRELIMINARY;  PRT;  501 AA.
AC   Q5RB70;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein DKFZp469E1839.
GN   Name=DKFZp469E1839;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   The German cDNA Consortium;
RA   Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR858784; CAH90990.1; -; mRNA.
```

us-10-063-518-14.spdl.rup

```
DR   SMR; Q5RB70; 204-385.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0008289; F:lipid binding; IEA.
DR   GO; GO:0008289; F:lipid binding; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   501 AA;  55355 MW;  3F3EEF2C413BD3BB CRC64;

Query Match             47.4%;  Score 566;  DB 2;  Length 501;
Best Local Similarity   51.2%;
Matches  123;  Conservative  31;  Mismatches  38;  Indels  48;  Gaps   6;

Qy      1 MNHLP-----------EDMENAL-------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV  51
          :  |  |          | : | :|      ||: | ::  :  ::   : : :::
Db      1 MSKLPRELTRDLEHSLPAVASLGSSLSHSQSLSSHLLLPPB------------KRRAISDV  49

Qy     52 RRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIPLLAVFRFKVL 111
          |||||||||||||||||||||||:::|
Db     50 RRTFCLFVTFDLLFISLLWIIELNV-----------------------LAFFRFSGL  83

Qy    112 ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
          :|||||||||||||:|:|||  |:||||||||||:|||:||:|||||||:|||||||||
Db     84 LLGYAVQRLQHWWVIAVTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL 143

Qy    172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK 229
          ||||||||||||||          |  ||:          ||||||||||||||||| :|::  :
Db    144 DFKVLPQEAEEERWYLAAQAAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVAGKK 203
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Job time : 301 secs

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